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Listing first 45 summaries
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# ALIGNMENTS

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                                                                                                                                                                                                                                  human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; Cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
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98.6%;
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RESULT 4
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XX BAC:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell with an effective amount of DNA or protein of the invention. Sequences AAU03841-AAU083897 represent Bacillus lipase
                                          human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory
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21-JUN-2001;
                                                                                                                                                Bacillus lipase polypeptide #4.
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                                                                                            animal feed; flavour modification; fat m
cheese; food emulsifier; leather tanning;
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98.1%;
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Pred. No. 9
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Bacillus lipase polypeptide #5

human foodstuff; cheese; food emulsifier; leather tanning; leather processing; cleaning agent; Crohn's disease; cystic

cystic fibrosis;

enzyme

Lipase; Bacillus; animal feed; flavour modification; fat modification;

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RESULT 6
AAU83846
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Best Local
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gastrointestinal
gastrointestinal.
               08-MAY-2002
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21-JUN-2001;
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               (first entry)
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2001US-300378P.
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lipid related condition; antiinflammatory; respiratory;
                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                               97.4%;
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                                                                                                                                                                                                                                                                                                                                                                                               Score 1060; DB 23;
Pred. No. 1.2e-100;
1; Mismatches 4;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
                                                                                                                                                                                                                                                                                                                                  Sequence
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21-JUN-2001; 2001US-300378P.
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disease; indigestion; obesity; gastrointestinal mal-absorption;
ntestinal lipid related condition; antiinflammatory; respiratory;
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                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                96.2%;
96.7%;
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Pred. No. 2.6e-99;
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RESULT 7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human foodstuff: cheese; food emulsifier: leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides of the invention.
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QIHGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
                                            QIHGVGHIGLEMNSQVNSLIKEGLNGGGQNTN 212
                                                                                                                                                                                                            GWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKYLDETGAKKVDIVAHSMGGANTPYYYKN
                                                                                                                  LDGGNKIENVVTLGGANRSTTSKALPGTDPNOKILYTSIYSSADMIVMNYLSKLDGAKNA 180
                                                                                                                                                                                   GWSRDKLYAVDFKDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKN
                                                                                            LDGGNKVENVVTLGGANRLTTGKALPGTDPNQKILYTSIYSSADMIVMNYLSRLDGARNV
                                                                                                                                                                                                                                                                                  MKFVKRRIIALVTILMLSVTSLFALQPSAKAAEHNPVVMVHGIGGASFNFAGIKSYLVSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 139; 196pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 AA;
                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointsstinal mal-absorption problems. Gastrointestinal lipid related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the invention. Seque polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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LDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNA
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                                                                                      GWSRDKLYAVDFWDKTGTNYNNGPVLPRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKN
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)B; ABK33820.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 138; 196pp; English.
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2001US-300378P.
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92.0%;
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                                                                                                                                                                                       The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohm's disease, Cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heather processing; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 138; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Giver LJ, Minshull J,
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21-JUN-2001; 2001US-300378P.
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                                                                                                                                                                                 polypeptides of the invention.
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                                                                                                           Similarity
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                                                                                            Score 1006; DB 23;
Pred. No. 4.2e-95;
3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            condition; antiinflammatory; respiratory
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                                                                                          Gaps
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GWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKN 120

Query Match
Best Local Similarity
Matches 196; Conserv

Conservative

6,

Mismatches

92.5%;

Score 1006; DB 23 Pred. No. 4.2e-95;

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Length Indels

212; 0

Gaps

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RESULT 10
AAU83855
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                                                                                     The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a mathed of badrolusing a limid corporation of a terract call or
                                                                                                                                                                                                                                                                                       Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
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                                           method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
                                                                                                                                                                                                                                                         Claim 32; Page 140; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUL-2001;
Sequence
                            polypeptides of the
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RESULT 11
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                                                                       acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAUB3841-AAUB3897 represent Bacillus lipase polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coellac disease.
                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUL-2000;
21-JUN-2001;
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                                                              polypeptides of the
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                                                              invention.
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N-PSDB;
          The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a matched of scan be therapeutically or prophylactically treated via a
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                                                                                                                                                              Claim 30; Page 140; 196pp; English.
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                                                                                                                                                                                                                                                                                                  LJ,
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the invention. Se
The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning.
                                                                                                                                                                                                                                                                                                                                                                             Lipase; Bacillus; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coellac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                            Claim
                                                                                                    Crohn's
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                                                                                                                             Nucleic
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                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                             5.
                                                                                                              acids encoding lipase enzymes al feeds, as agents of flavour
                                                                                                    disease and coeliac disease -
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                                                                                                                                                                                                               MAXYGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein; 180
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                                                                                                                                                                                      Minshull J,
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                                                                           145-146; 196pp;
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                                                                                                                                                                                      Vogel
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                                                                            English.
                                                                                                              which are use modification
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ion and
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     cleaning
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
                                                              Claim
                                                                                                       'n
                                                                                                                                                                                  Giver LJ,
                                                                                                                                                                                                                                   13-JUL-2000;
21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides of the invention.
                                                                                                                                                                                                         (MAXY-)
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                                                                                                  cleic acids encoding lipase enzymes animal feeds, as agents of flavour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              They are also useful for treating Crohn's disease s, coeliac disease, indigestion, obesity and other
                                                                                        disease and
                                                                                                                                                                                                          MAXYGEN INC
                                                                                                                                             ABK33868
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                                                              Page 145;
                                                                                                                                                                                  Minshull
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98.3%;
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                                                                                                   which are useful modification and
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The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food

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RESULT 15
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The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements animal feeds, as agents of flavour modification and fat modification in
                                                                                                                                                                      Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
                                                                                                                   Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                     Giver LJ,
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21-JUN-2001; 2001US-300378P
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DB; ABK33862.
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                                                                                                             Page 144; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                               Minshull J,
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97.88;
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Pred. No. 1.8e-86;
2; Mismatches 2;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          polypeptides of the invention.
                                                                                      153 KILYTSIYSSADMIVMNYLSKLDGAKNAQIHGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
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                                                                                                                                                       VLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQ
                                                                    KILYTSIYSSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
                                                                                                                                      VLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQ
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97.28;
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Pred. No. 3.7e-86;
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Maximum
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  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
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US-09-134-001C-4054
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US-08-111-556A-3
US-09-134-001C-3517
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US-08-286-870A-4
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US-09-509-814A-6
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US-07-930-678-2
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671 2 US 551 4 US 312 4 US 11073 4 US 11073 4 US 284 4 US 316 1 US 539 4 US 539 4 US 539 4 US 340 4 US 340 4 US 371 3 US 371 4 US
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US-08-737-716-13 5472855-5 US-09-615-192A-348 US-09-615-192A-3465 US-09-206-942-49 US-09-206-942-47 US-09-134-001C-2927 US-09-134-001C-2927 US-09-134-001C-4056 US-09-134-001C-4412 US-09-134-001C-4412 US-09-134-001C-4412 US-09-138-574A-43 US-09-134-001C-4412 US-09-134-001C-4412 US-09-134-001C-4412 US-09-138-574A-43 US-09-138-574A-43 US-09-134-001C-4412 US-09-134-001C-4412 US-09-138-574A-43 US-09-138-347-34

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Best Local :
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                                                                                                                                          NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                      TOPOLOGY: 11
                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acid
                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PN TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Kokulis Dan' "
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                               NAME: Kokulis, Paul N
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/727,235 FILING DATE: 03-JUL-1991
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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6714627 CUSH
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                                                                                                              358 amino acids
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                                                                                                                                                                                      (202) 861-3000
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           12.8%;
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 26; Mismatches
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Pred. No. 3.7e-79;
             Score 139.5; DB 1; Pred. No. 5.6e-07;
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Gaps
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Patent No. 5804409
                                                                                                                                                      Query Match 12.8%; Score 139.5; DB 1
Best Local Similarity 29.6%; Pred. No. 5.6e-07;
Matches 48; Conservative 26; Mismatches 59
                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 822-094
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 03-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,015
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Kokulis, Paul N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 ATKVNLIGHSQGGLTSRYVA--AVAPQLVASVTTIGTPHRGS 156
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                                     49
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ZIP: 20036-5601
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61 KFANVVDYWYGIQSDLQSHG---AKVYVANLSGFQSDDGPN-GRGEQLLAYVKQVLAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kokulis, Paul N
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                             N
                                                                                                                1 MKFVKRRIIALVTILVLSVTSL-----FAMQPSAKAAE-----HNPVVMVHGIGGASY 48
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                                 NFA-----GIKSYLVSQGWSRGKLYAVD---FWDKTGTNYNNGPVLSRFVQKVLDETG 98
                                                                           VRSMRSRVAARAVAWALAVMPLAGAAGLTMAASPAAVAADTYAATRYPVILVHGLAGTD- 60
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                                                                                                                                                                                                                                                                                                                       358 amino acids
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VISSER, Christiaan
VISSER, Christiaan
VISSER, Christiaan
VERTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
VENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
VENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
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FRENKEN, Leon G
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                               US-09-336-601-1
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                                                                                                                                           Sequence 1, Application US/09336601 Patent No. 6184008
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 2, Application US/08978589A Patent No. 6087145
                                                                                                                          GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
         APPLICANT: ISHII, Takeshi
APPLICANT: MITSUDA, Satoshi
TITLE OF INVENTION: PRODUCTION OF OPTICALLY ACTIVE SPHINGOID COMPOUND
                                                                 APPLICANT: OHTA, Hiromichi
APPLICANT: SUGAI, Takeshi
APPLICANT: ISHII, Takeshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 205-80:
INFORMATION FOR SEQ ID NO:
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 CURRENT
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APPLICANT: MITSUDA, Satoshi
APPLICANT: MITSUDA, SATOSHI
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                    138
                                                                                                                                                                                                                                                                                    116 YYIKNLDGGNKIENVVTLG----GANRSTTSKALPGTDP 150
                                                                                                                                                                                                                                                                                                                                                            65 -----GKLYAVD---FWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                13 TILVLSVTSLFAMQPSAK-----AAEHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                        80 DLRAHGAAVYVANLSGFQSDDGPN-GRGEQLLAFVKQVLAATGAQKVNLIGHSQGGL-TS 137
                                                                                                                                                                                                                                                                                                                                                                                                26 TVLAMSLAGAQAASAATTAVDDYAATRYPIILVHGLTGTD-KYGGVVEY-----WYRIPE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                   RYVASV-APELVASVTTISTPHWGSQFADFVQQLLQTDP 175
APPLICATION NUMBER: US/09/336,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
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FALLS CHURCH
VIRGINIA
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SYSTEM: PC-DOS/MS-DOS
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ID NO: 2:
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Pred. No. 3.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-03-03 NUMBER OF SEQ ID NOS: 2
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                             REFERENCE/DOCKET NUMBER: 36,728
REFERENCE/DOCKET NUMBER: 36,171
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                       FILING DATE: 20-DEC-1991 PRIOR APPLICATION DATA:
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                                                                                                    ATTORNEY/AGENT INFORMATION:
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                  TELEPHONE:
                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 25-MAR-1993
                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                          FILING DATE:
                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VKRRIIALVTILVL-----SVTSLFAMQPSAK-----AAEHNPVVMVHGIGGA 46
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    Application US/08400422
    5681715

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10174-6201
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                                                                                     Lambiris,
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212 867 0298
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25.0%;
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Pred. No. 4.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LYNN DOUCETTE-Stamm et al
APPLICANT: LYNN DOUCETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 3301
LENGTH: 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR EILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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ORIGINAL SOURCE:
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HYPOTHETICAL: N
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ORGANISM: PSG...
OMBAIN: DSM 3401
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                   196 KQGKPSRMNAAYRQLLSLYKIYCGKEIEVLNIYGDLEDGSHSD-----
                                               143 KALPGTDPN----QKILYTSIYSSADMIVMNYLSKLDGAKNAQIHGVGHIGLLMNSQVNS 198
                                                                                 136 FGIQQENEVGHSMGNISFAFYMKNYGDDRHLPQLKKEVNIAGVYNGILNMNENVNEIIVD 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 42; Conserv
                                                                                                                   97 TGAKKVDIVAHSMGGANTPYYIKNLDGGN---KIENVVTLGG----
                                                                                                                                                    76 VTNEVITARVSSEGKVYFDKKLSEDAANPIVKVEFKDNKTGNFKENAYWIKEVLSQLKSQ 135
                                                                                                                                                                                         63
                                                                                                                                                                                                                                                       13 TILVLSV-----TSLFAMQPSAKAAEHNPVVMVHGIGGASYNFAGIKSYLVSQGW--- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 TGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 D-KYAGVLEYWYGIQEDLQQHG---ATVYVANLSGFQSDDGPN-GRGEQLLAYVKTVLAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 SYNFAGIKSY-----LVSQGWSRGKLYAVD---FWDKTGTNYNNGPVLSRFVQKVLDE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                       20 TVLVLVIIYNKTQSQSYISTHYSNNKIKTTATLFLHGYGGSERS----ETFMVKQALNKN 75
                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VKRRIIALVTILVLSV-----TSLFAMQPSAKAAEH----NPVVMVHGIGGA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGATKVNLVGHXQGGLTSRYVA--AVAPDLVASVTTIGTPHR 159
                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301, Application US/09134001C
6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                           9.0%; Score 97.5; DB 4;
19.9%; Pred. No. 0.016;
tive 38; Mismatches 90;
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Pred. No. 0.00035;
                                                                                                                                                                                      -----AVDFWD-KTGTNYNNGPVLSRFVQKVLDE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                            Length 292;
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                                                                                                                   ----ANRSTTS 142
               -- GRVSNSSSQS 248
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                                                                                                                                                                                                                                                                                             65;
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                           9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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US-09-134-001C-4568
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 4568,
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LENGTH: 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
 Matches
                                                                                                                                                                                                                                                                                                                                                           Patent No.
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Best Local Similarity
Matches 54; Conserv
                            Query Match
                                                                                                 LENGTH: 690
TYPE: PRT
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; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4568
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                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4568
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 GTHASDLLG --- NEAIVRQLAYD ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 HSMGGANTPYYIKNLD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 I-SAFGSNYDRAVELYYYIKGGRVDYGAAHAAKYGHERYGKTYEGVYKDWKPGQKIHLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 SAKQKQYKNNDPIILVHGFNGFTDD---INPSYLTHYWGGDKMNIRQDLEENGYEAYEAS 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNAQI-HGVGHIGL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSMGGQT----IRQLEELLRHGNPEEVEYQKQHGGEISPLFQGGHDNMVSSITTLGTPHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FWDKTGTNYNNGPVLSRFVQKVLDETGA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09134001C
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     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       1998-08-13
                       8.4%; Score 91.5; DB 20.4%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.5%; Score 92; DB 4; Length 699; 19.7%; Pred. No. 0.23;
     32;
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     Mismatches
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                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GG--NKIENVVTLGGANR 138
                                                      Length 690;
  Indels 107;
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Gaps
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                                 Matches
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                                                                                                                                                                                         NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                            TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                        'ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531 IWNTEDQAVNDLTTQGAEKINQQTS 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 -RKLVKETI-----NRIGRLSGGKDVDIDLGFSQWGLKQQPNESYIDYAERVSKSK 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   423 ROMEEFLRNGNQEEIEYQRQHGGTISDLFTGGKDNMVASITTLGTPHNGTPAADKIGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 YDRAVELYYYVKGGRVDYGAAHAAKYGHHRYGRTYKGIMRDWEPGKKIHFIGHSMGGQTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 PVVFVHGFLGFAGDNQFSLAPKYWGGTKYN---IDRNLTNEGYNVHEANIGAF----SSN
                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 YNNGPVLSRFVQKVLDETGA--
                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                  NAME: Oblon, No. 5306633man F. REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 PVVMVHGI---
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
2 KFVKRRIIALVTILVLSVTSLFAMQPSAKAAEH-----NPVVMVHGIGG-ASYNFAG
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                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22202
                                                                                                                                         amino acid
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                                                                                                                                                        213 amino acids
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                                                                                                                                                                                                                          (703) 413-2220
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
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                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                        (703) 413-3000
                                           8.1%;
25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08/104445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAKING AGENTS CONTAINING A XYLANASE, AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIAL XYLANASE, PRODUCTION, BACTERIA ENCODING A XYLANASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERWIN
                                                                                                                                                                                                                                                                                                                                                                   08/104,445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BRUNO
                               24;
                                                                                                                                                                                                                                                                           583-179-0
                                             Score 88;
Pred. No.
                                              Pred
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                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                   Version
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                                                            Length
                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XYLANASE, DNA FRAGMENT
                              38;
                            Gaps
52
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: EP 9. FILING DATE: 04-MAY-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM
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118 IKNLDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGA 177
                                                                                                                                                                           Local
                                                                                                                          13 TILVLSVTSLFAMQPSAKAA-----EHNPVVMVHG-----IGGASYNFAGIKSYL
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                               65 RSDGAS---VYITEV-SQLNTSELRGEELLEQVEEIAAISGKGKVNLVGHSHGGPTVRYV 120
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                                                             VSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYY 117
                                                                                             TLLALCIGSSLLLSGPAEAGLFGSTGYTKTKYPIVLTHGLLGFDSILGVDY-WYGIPSSL
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52; Conserv
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Gerritse, Gijsbert
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GENERAL INFORMATION:

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RESULT 13
US-08-456-956-2
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US-08-232-519-2
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Sequence 2, Application US/08456956 Patent No. 5686285
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REFERENCE/DOCKET NUMBER: SH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
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                                                                                                   248
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                                                                                                                                   135 GANRSTTSKALPGTDPNQKILYTSIYSSA-----DMIVMNYLSKLDGAKNA 180
                                                                                                                                                                                                                                   134 EGTPIVLVHGEGG-----DISNWLLTQDALAAERRVIAFDLPGHGASSKNVGTGTLAFL 187
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                                                                                                                                                                                                  87 SRFVQKVLDETGAKKVDIVAHSMGGA------NTPYYIKNLD-----GGNKIENVVTLG 134
                                                                                                                                                                                                                                                                     33 EHNPVVMVHGIGGASYNFAGIKSYLVSQG--WSRGKLYAVDFWDKTGTNYNNG----PVL 86
                                                                                                                                                                                                                                                                                                      Local Similarity
nes 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 5-96286 FILING DATE: 22-APR-1993
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                                                                                                   AFVDSESSRDM-----KAVLQMLVYNKALVGRKMVDAVLR--ARRLDGARDA
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Pred. No. 0.3;
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                                                                                                                  GENERAL INFORMATION:
                                                                                                                                   Sequence 3517, App
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.0%;
Best Local Similarity 23.1%;
Matches 40; Conservative 3
          FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION: EPIDERMIDIS FOR
PRIOR APPLICATION NUMBER: US 60/064,964
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
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NAME: Haley Jr, James F
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APPLICATION NUMBER:
FILING DATE: 22-APR-
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                                                                                                                                                                                                                                                                         GANRSTTSKALPGTDPNQKILYTSIYSSA-----DMIVMNYLSKLDGAKNA 180
                                                                                                                                                                                                                                                                                                             AGVVSELLQTLKIEKAHVVGHSLGGGIALTLLRDHPDQVASLNLLAPAGLGKDVNADFIS
                                                                                                                                                                                                                                                                                                                                                                              EGTPIVLVHGFGG-----DISNWLLTQDALAAERRVIAFDLPGHGASSKNVGTGTLAFL 187
                                                                                                                                                                                                                                                                                                                                            SRFVQKVLDETGAKKVDIVAHSMGGA-----NTPYYIKNLD-----GGNKIENVVTLG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                      Application US/09134001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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PC-DOS/MS-DOS
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Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHGN-4 DIV
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                                                                  AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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8

SEQ ID NO 3517

PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US: 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674

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RESULT 15
US-09-111-556A-3
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; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 21.4 Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                                                       TELEPHONE: 212-867-0123
                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK PCT/DK93/00225
FILING DATE: 03-JUN-1993
                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Clausen, Ib G
APPLICANT: Hansen, Mogens T
TITLE OF INVENTION: C. ANTAH
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 GT----PAAD---KLGSTKFIKD----TINRIGKIGGTK 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 HLVGHSMGGQTIRLMEHFLRNGNQEEIDYQRQYGGTVSDLFKGGQDNMVSTITTLGTPHN 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 DIVAHSMGGAN---TPYYIKN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 NVGAF----SSNYDRAVELYYYIKGGRVDYGAAHAAKYGHKRYGRTYEGIMPDWEPGKKI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 QLTAQAQYKNQYPVVFVHGFVGLVGEDAFSMYPNYWGGTKYN---VKQELTKLGYRVHEA 316
                                                                                              REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 22-DE
                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 YAVDFWDKTGTNYNNGPVLSRFVQKVLDETGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 QPSAKAAEHN--PVVMVHGI------GGASYNFAGIKSYLVSQGWSRGKL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAK 178
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                                                                                                                           Lambiris, Elias J
                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 Lexington Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Svendsen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borch, Kim
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Egel-Mitani, Michi
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'ARR: 3748.214-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 87; DB 4;
Pred. No. 0.74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LDGG--NKIENVVTLGGANR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 652;
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; TYPE: amino acid; STRANDEDNESS: single; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-111-556A-3
Search completed: May
Job time : 16 secs
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                                                                                                                                                                                                                Query Match 8.0%;
Best Local Similarity 26.4%;
Matches 29; Conservative 21
                                                                       66
                                                                                                         91 OKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRST 140
                                                                                                                                             10 PILLVHGLFGFDRIGSHHYFHGIKQALNECGAS----VFVPIISAANDNEARGDQLLKQI 65
                                                                                                                                                                               36 PVVMVHGIG-----GASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFV
                                                                       HNLRRQVGAQRVNLIGHSQ-GALTARYVAAI-APELIASVTSVSGPNHGS 113
                  9, 2003, 16:22:45
                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                   Score 86.5; DB 3; Pred. No. 0.23;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                       101.5
92.5
89.5
89.5
87.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
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86.5
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Gapop 10.0 , Gapext 0.5
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1088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9, 2003, 16:22:01 ; Search time 20 Seconds (without alignments) 975.473 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US0_NEW_PUB.pep:*
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9 US-10-147-467-2

9 US-10-147-467-2

12 US-10-080-644-6

10 US-09-815-242-5111

10 US-09-815-242-11886

10 US-09-815-242-11886

10 US-09-912-020-281

10 US-09-912-020-281

10 US-10-098-174-1

12 US-10-098-174-1

12 US-10-098-174-1

12 US-10-098-174-1

13 US-10-098-174-2

14 US-10-098-174-2

15 US-10-098-174-3

16 US-10-098-174-3

17 US-10-098-174-3

18 US-10-098-174-3

19 US-10-098-174-3

10 US-10-09
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   US-09-884-696-5
US-09-738-626-3604
US-09-813-408-12
US-10-108-605-65
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                                                  Sequence 4, Appli
Sequence 3594, Ap
Sequence 3594, Ap
Sequence 2, Appli
Sequence 6, Appli
Sequence 5111, Ap
Sequence 11886, Appli
Sequence 281, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 35, Appl
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Sequence
Sequence
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45	44	43	42	41	40	39	38	37	36	35	34	ω w	32	31	30	29	28	27	26	25	24	23	22	21	20
74	74.5	74.5	74.5	74.5	74.5	75	75	75	75.5	. 76	76	76	76	76	76	76		76.5	77.5	77.5	78	79	79	79	79
б. 8						6:9					7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.1	7.1	7.2	7.3	7.3	7.3	7.3
184	363	274	274	274	274	1781	535	297	380	434	357	280	275	275	275	275	372	254	1093	495	503	1463	871	836	235
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US-09-734-017A-78	US-09-797-464A-11	US-09-060-854B-5	US-10-033-325-5	US-09-813-408-17	US-08-322-678-9	US-09-995-749A-2	US-09-995-749A-13	US-10-080-644-7	US-09-813-408-16	US-09-971-536-62	US-09-837-235-15	US-09-731-872-314	US-09-060-854B-4	US-10-033-325-4	US-09-813-408-18	US-08-322-678-8	US-09-813-408-9	US-10-080-644-5	US-09-801-368-392	US-10-213-990-42	US-10-211-962-64	US-09-971-536-69	US-09-858-525A-2	US-09-858-525A-10	US-09-533-029-74
e 78,	Ξ.	е 5	5,	17,	9	2, 1	ω,	e 7,	16,	73	Sequence 15, Appl	Sequence 314, App	Sequence 4, Appli	Sequence 4, Appli	Sequence 18, Appl	φ,	D	5, N	e 392	42,	64,	~	Sequence 2, Appli	`	Sequence 74, Appl

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                                                                                                                                                                                                                           Query Match 97.4%;
Best Local Similarity 97.6%;
                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Methods and Compositions for Developing Spore Display
TITLE OF INVENTION: Systems for medicinal and Industrial Applications
FILE REFERENCE: 18097A-033520US
CURRENT FILING DATE: 2001-12-19
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/214,161
PRIOR APPLICATION NUMBER: US 60/214,161
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 09/892,208
PRIOR FILING DATE: 2001-06-26
NUMBER OF SED ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Bacillus circulans
                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 212
121 LDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNA 180
                                                                                                                   GWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKN 120
                                       GWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKN
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Longchamp, Pascal F.
Whalen, Robert G.
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                       Score 1060; DB 12
Pred. No. 6.9e-97;
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                                                                                                                                                                                                                                              DB 12;
                                                                                                                                                                                                                                            Length 212;
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US-09-738-626-3593
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                                                                                                                                                                                                                                                                                                                                  RESULT 3
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn ver. 3.0 SEQ ID NO 3593 LENGTH: 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3593, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                             Sequence 3594, Application US/09738626 Publication No. US20020197605A1
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                       APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
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                                       TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                              APPLICANT:
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IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                             OCHIAI, KEIKO
YOKOI, HARUHIKO
                                                                         IKEDA, MASATO
OZAKI, AKIO
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                                                                                                       TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                                                                                                                      ANDO, SEIKO
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Pred. No. 1.9e-07;
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US-10-147-467-2
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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LENGTH: 300
TYPE: PRT
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 363
TYPE: PRT
Sequence 6, Application US/10080644
Patent No. US20020137172A1
GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 2002-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TAKESHI, IShii
APPLICANT: SATOSHI, Mitsuda
TITLE OF INVENTION: ESTERASE GENE AND
FILE REFERENCE: 20-4336P
                                                                                                                                                138 RYVASV-APELVASVTTISTPHWGSQFADFVQQLLQTDP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 SKALPGTDPNQKILY 156
                                                                                                                                                                                         116 YYIKNLDGGNKIENVVTLG----GANRSTTSKALPGTDP 150
                                                                                                                                                                                                                                                                                                                                       13 TILVLSVTSLFAMQPSAK-----AAEHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR--- 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPV-----LSRF 89
                                                                                                                                                                                                                                 DLRAHGAAVYVANLSGFQSDDGPN, GRGEQLLAFVKQVLAATGAQKVNLIGHSQGGL-TS 137
                                                                                                                                                                                                                                                                       -----GKLYAVD----FWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTP 115
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27.0%;
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Pred. No. 0.0004;
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APPLICANT: Glucksmann, Maria, Alexandra

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; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-080-644-6
                                                                                                             ; ORGANISM: Pseudomonas aeruginosa US-09-815-242-5111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 299
                                        Matches
                                                         Query Match
Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                  TYPE: PRT
                                                                                                                                                                LENGTH: 1062
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3 FVKRRIIALV---TILVLSVTSLFAMQPSAKAAEHNPVVMVHGIGGASYNFAGIKS----
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                                                                                                                                                                                   NO 511:
                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                         FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                        FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/207,727
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o. US20020061569A1
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Zyskind, Judith W.
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ilarity 25.3%;
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Pred. No. 1.8;
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Pred. No. 0.0
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US-09-815-242-11886
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                                                        TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Glucksmann, Maria, Alexandra et al. TITLE OF INVENTION: 33167, A NOVEL HUMAN HYDROLASE FILE REFERENCE: MNI-140
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CURRENT FILING DATE: 2002-02-22
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TYPE: PRT
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APPLICATION NUMBER: 60/242,578
                                       APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLLTYHGLFGSKQNWRGISKALVRK-VSR-KVYAIDVRNHGESPHSSVHNSKAMSEDLRL 111
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Yamamoto, Robert T.
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Zyskind, Judith W.
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Pred. No. 0
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US-09-815-242-11886
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US-09-912-020-281
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SOFTWARE: FastSEQ for
SEQ ID NO 281
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Best Local Similarity
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PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
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CURRENT FILING DATE: 2001-07-23
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PRIOR FILING DATE: 2000-12-22
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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415 AGISAGDRVVTDGIDRLTEGAK 436
                                    158 SIYSSADMIVMNYLSKL-DGAK 178
                                                                                                                                             297 VVQAQKAGKPLVVEAWDRTNSKKLSEGTLLS--LDNQIDATTGTIKVKARFNNQDDALFP 354
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                                                                       NQFVNARMLVDTEQNAVVIPTAALQMGNEGHFVWVLNSENKVSKHLVTPGIQDSQKVVIR 414
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US20020045592A1
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Forsyth, R. Allyn
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Pred. No. 1.
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US-10-080-644-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Staphylococcus epidermidis US-10-098-174-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-10-098-174-1
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LENGTH: 518
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 21.4
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10098174 Patent No. US20020169288A1 GENERAL INFORMATION:
                                                                                                                    Matches
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10080644 Patent No. US20020137172A1
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/584,568 PRIOR FILING DATE: 2000-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/275,718 PRIOR FILING DATÉ: 2001-03-15 NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HOOK, Magnus
APPLICANT: BOWDEN, Maria
TITLE OF INVENTION: COLLAGEN-BINDING ADHESIN FROM STAPHYLOCOCCUS EPIDERMIDIS.
FILE REFERENCE: P07136US01/BAS
                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/080,644
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Glucksmann, Maria, Alexandra et al.
TITLE OF INVENTION: 33167, A NOVEL HUMAN HYDROLASE AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/098,174
CURRENT FILING DATE: 2002-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: MNI-140
                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                       LENGTH: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 STTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 NVGAF----SSNYDRAVELYYYIKGGRVDYGAAHAAXYGHKRYGRTYEGIMPDWEPGKKI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 HLVGHSMGGQTIRLMEHFLRNGNQEEIDYQRQYGGTVSDLFKGGQDNMVSTITTLGTPHN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 DIVAHSMGGAN---TPYYIKN--
                                         69
                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 QLTAQAQYKNQYPVVFVHGFVGLVGEDAFSMYPNYWGGTKYN---VKQELTKLGYRVHEA 150
  89 FVQKVLDETGAKKVDIVAHSMGG 111
                                                                             37 VVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGP------VLSR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 YAVDFWDKTGTNYNNGPVLSRFVQKVLDETGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 QPSAKAAEHN--PVVMVHGI-----
                                     VVFLHGLFGSKTNFNSIAKILAQQTGRR--VLTVD--
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                                                                                                                    Conservative
                                                                                                                                       8.0%;
30.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 87;
21.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                  2002-02-
                                                                                                                  13;
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                                                                                                                                     Score 86.5; D
Pred. No. 1.3;
                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9; Length 518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
                                       -ARNHGDSPHSPDMSYEIMSQ 121
                                                                                                                                                          12;
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                                                                                                                    Indels
                                                                                                                                                          Length
                                                                                                                                                            315;
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                                                                                                                   RESULT 13
US-10-027-805-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Staphylococcus aureus US-09-815-242-5841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-815-242-5841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 5841
LENGTH: 690
                                                               Sequence 35, Application US/10027805 Patent No. US20020164725A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Haselbeck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITLE OF INVENTION: Identification of Essential Genes in ITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IOR APPLICATION NUMBER: 60/206,848 IOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                     422 EEFLRNGNKEEIAYHKAHGGEISPLFTGGHNNMVASITTLATPHNGSQAADKFGNTEAVR
                                                                                                                                                                                                                                                                                                                                                                                                                 306 PVVFVHGFLGLVGDNAPALYPNYWGGNKFKVIEELRKQGYNVHQASVSAF----GSNYDR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 DLQDLLPQLGLVPCVVVGHSMGG 144
                                                                                                                                                                                            482 KIMFALNRFMGNKYSNIDL 500
                                                                                                                                                                                                               153 KILYT-----SIYSSADM 165
                                                                                                                                                                                                                                                                                                       118 IKNLDGGNKIE------NVVTLGGANR---STTSKALP----
                                                                                                                                                                                                                                                                                                                                          362 AVELYYYIKGGRVDYGAAHAAKYGHERYGKTYKGIMPNWEPGKKVHLVGHSMGGQTIRLM 421
                                                                                                                                                                                                                                                                                                                                                                              83 GPVLSRFVQKVLDETGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 PVVMVHGIGG------ASY-NFAGIKSYLV-----SQGWSRGKLYAVDFWDKTGTNYNN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23 APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5841, Application US/09815242
o. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/815,242 FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto, Robert T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
MURPHY, L.
                                              ROBERTSON, Daniel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.0%;
24.1%;
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                          Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 86.5;
Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73;
                                                                                                                                                                                                                                                                                                   --GTDPNQ 152
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US-10-027-804-35
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                                                                                                                                                                       Sequence 35, Application US/100 Publication No. US20030054530A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619-678-5099 INFORMATION FOR SEQ ID NO: 35: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     128 LHRI--GYPLAKILASIAYKKSSRLV----ADLSFGKNA 160
                                                                                                                                                                                                                                                                                                                                        142 SKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            70 RFENFISDLDAVVRETGVEKFVLVGHSFGTMISMKYCS--EYRNRVLALILIGGGSRIKL 127
                                                                                                                                                                                                                                                                                                                                                                                                               88 RF-----VQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 PIVFVHG-WTANMNF------WKEQRRYFAGRNMMLFVDNRGHGRSDKPLGYDFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVD----FWDKTGTNYNNGPV---LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 09010/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, STE 1400
       TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ESTERASES
                                                                                                                                                     APPLICANT: ROBERTSON, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 262 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: HAILE, LISA A. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/602,359 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/027,805 FILING DATE: 21-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CALIFORNIA
                                                                                                                                                                                                         Application US/10027804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF SEQUENCES:
                                                                                                               MURPHY, Deni
REID, John
                     SWANSON, Ronald V. WARREN, Patrick V. KOSMOTKA, Anna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAFFIA,
LINK, St
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                                                                                  LINK,
                                                                                              MAFFIA,
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                                                                          Steven
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                                                                                              Anthony
                                                                                                                                    Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 85; DB 9;
Pred. No. 1.5;
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87

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NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C

4225 EXECUTIVE SQUARE, STE 1400

CITY: LA JOLLA STATE: CALIFORNIA

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                                                                                                                                                                                                                                                                                                                                    Sequence 35, Application US/09903410
Patent No. US20020146799A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
CURRENT APPLICATION NUMBER: US/09/903,410 CURRENT ETILING DATE: 2001-07-10 PRIOR APPLICATION NUMBER: US 09/382,242 PRIOR FILING DATE: 1999-08-24
                                                                               APPLICANT: KOSMOTKA, ADDA TITLE OF INVENTION: ENZYMES HAVING ESTERASE ACTIVITY AND METHODS OF USE THEREOFFILE REFERENCE: DIVER1180-2
                                                                                                                                                                                                                                                                           APPLICANT: DIVERSA CORPORATION
APPLICANT: ROBERTSON, Dan
                                                                                                                                                                       PPLICANT:
                                                                                                                                                                                                                 PPLICANT:
                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 35: SEQUENCE CHARACTERISTICS:
                                                                                                                                                      PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 LHRI--GYPLAKILASIAYKKSSRLV----ADLSFGKNA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 SKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 RFENFISDLDAVVRETGVEKFVLVGHSFGTMISMKYCS--EYRNRVLALILIGGGSRIKL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 PIVFVHG-WTANMNF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVD-----FWDKTGTNYNNGPV---LS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 25.2 les 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                       INFORMATION:
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                                                                                                                                           LINK, Steven
SWANSON, Ronald
WARREN, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/602,359 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 262 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: HAILE, LISA A. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/027,804 FILING DATE: 21-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.
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                                                                                                                                                                                                                                   MURPHY, Dennis
REID, John
                                                                                                                                                                                                               MAFFIA,
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25.2%; Pre
25.2%; 23;
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Matches 40; Conserva
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                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                    TYPE: PRT
128 LHRI--GYPLAKILASIAYKKSSRLV----ADLSFGKNA 160
                                 142 SKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNA 180
                                                                                                                                                     36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVD----FWDKTGTNYNNGPV---LS 87
                                                                  70 RFENFISDLDAVVRETGVEKFVLVGHSFGTMISMKYCS--EYRNRVLALILIGGGSRIKL 127
                                                                                               88 RF-----VQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTT 141
                                                                                                                                22 PIVFVHG-WTANMNF-----
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Pred. No. 1.5;
23; Mismatches
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Gaps

Search completed: May Job time : 22 secs 9, 2003, 16:29:38

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Maximum
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB
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1088
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PIR_73:*
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lipase lipB -
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31	104.5	9 . 5 6	237	N	T26660	hypothetical prote
	101.5	9.3	299	2	T23932	
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	97.5	9.0	268	2	S73694	triacylglycerol li
35 5	97.5	9.0	1519	2	S41525	major ring-forming
36	96.5	8.9	1335	N	T17508	glycoprotein Vp260
37	96	8.8	377	2	A82713	triacylglycerol li
38	94.5	8.7	438	2	в83295	
39	94	8.6	267	N	F90516	esterase/lipase 1
40	94	8.6	688	ν	A47705	triacylglycerol li
41	93.5	8.6	272	Ν	E97008	periplasmic amino
42	w	8.6	638	N	AH0340	putaive autotransp
ω.	93	8.5	682	Ν	\$68970	triacylglycerol li
44	92.5	α.	1062	N	F83335	RND multidrug effl
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SULT 1 3934 pase li	SULT 1 3934 pase lipA - Bacil Species: Bacillus	_	us subtili	S		
Date: 2 Accessi	Date: 22-Nov-1993 # Accession: S23934;	••	sequence B69652	re	#sequence_revision 10-Nov-1995 #te B69652	#text_change 15-Oct-1999
Dartois, V.; ochim. Biophy	, V.; Baulard, A.; Biophys. Acta 1131,	Baulard, A.; s. Acta 1131	t n	tha 253	Schanck, K.; Colson, C. 253-260, 1992	
Title:	Title: Cloning, n	nucleotide	cleotide s	eq		n Escherichia coli of a lip
Accession:	on: \$23934					•

C.Date: 22-Nov 1993 Secquence\_revision 10-Nov-1995 #text\_change 15-Oct-1999
C.Accession: \$3394; B69652
R.Dartols, V.; Baulard, A.; Schanck, K.; Colson, C.
Blochim. Blophys. Acta 1131, 253-260, 1992
A.Title: Cloning, nucleotide sequence and expression in Escherichia coli of a lipase A. Reference number: \$32934; MUID:92329338; PMID:1320940
A.Accession: \$23934
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-212 < CAR>
A.; Cross-references: GB.M74010; NID:9143153; PIDN:AAA22574.1; PID:9143154
A.; Cross-references: GB.M74010; NID:914410; NID:914410

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61 61

GWSRGKLYANDEWDKTGTNYNNGPVLSRFYQKYLDETGAKKYDIVAHSMGGANTPYYIKN 120

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M.; Shen, M.; Vamathevan, J.J.; Lam, P.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                   R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, I.M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald,
                                                                                                         probable lipase -
C;Species: Deinocc
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C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision
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  A; Title: Genome sequence of the radioresistant bacterium A; Reference number: A75250; MUID:20036896; PMID:10567266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12664.1; A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-210 <KUN>
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C;Species: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                            ;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000;Accession: G75316
                                                                                                         Species: Deinococcus radiodurans
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                                                                                                                                                                                    LYGIGHIGLLSNSQVNGYIKEGLNGGGLNTN
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                                                                                                                                                                                                                                                                                        WQSNKLYAIDFYDKTGNNLNNGPQLASYYDRYLKETGAKKYDIVAHSMGGANTLYYIKYL 119
                                                                                                                                                                                                                                                                                                                                           MKKVLMAFIICLSL-ILSVLAAPPSGAKAESVHNPVVLVHGISGASYNFFAIKNYLISQG
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity.
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                   Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                       67.2%;
68.2%;
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Pred. No. 1.6e
23; Mismatches
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T.; Zalewski,
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              radiodurans
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A; Residues: 1-290 <SAU>
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                                                                                                                                                                                                                                                                                                                              SCOEDB: SCI11.24c
                                                                                                                                                                                                                                                                           1 Similarity
57; Conserv
 protein sll1969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T36757
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C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: G75316
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-237 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Saunders, D.; Harris, D.; James, K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable secreted lipase - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                   23 FAMOPSAKAAEHNPVVMVHGIGGASY-NFAGIKSYLVSQGWSRGKLYAVDFWDKTGTN--
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                                                                                                                                                                                                           YNNGPV-----LSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTL 133
LATKYDEVVTPYRGQFLDG
                                          IYSSADMIVMNYLSK-LDG
                                                                                                                                    GGANRSTT----SKALP----
                                                                                                                                                                              HGLGPVEKSAEQLAAHVDKVLAATGATETDLVGHSQGGMMPRYYLKFLGGAAEVNALVGI
                                                                                                                                                                                                                                                                           YTCKPS--AAHPRPVVLVHGTFGNSVDNWLGLAPYLKNRGYC---VFSLDYGQLPGVPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RYATWWSPCDAVINPNSSVPLSGATNTKTSCLTHSSLYGDATVYTQVRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RYYLKNLGGTAKVDAWVSLGGPNHGTDFALACSTASCIEMRQGSSFIKALNSGDETPGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYYIKNLDGGNKIENVVTLGGANR ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAFSKRFVLLPLSAALLAGCGTLTQAPSELSAQALAAPVRHPVLFVHGFNSDGSIWSPMM
                                                                                       APSNHGTTLSGLTRLLPYFPGAEDLLNEHTPALADQVVGSDVLTRLNAGGDTVPGVRYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source: strain
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL:AL096849; PIDN:CAB50950.1; GSPDB:GN00070; SCOEDB:SCI11.24c
                                                                                                                                                                                                                                                                                                                                                                                     16.4%;
28.6%;
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Pred. No. 5.7e-10;
7; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                     Score 178; DB 2;
Pred. No. 2.3e-07;
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1999
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 290;
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Synechocystis sp.

(strain

PCC

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hypothetical protein Y38E10A.g - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C:Accession: T26657
R:Wallis, J.
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AL110484; PIDN:CAB54398.1; CESP:Y38E10A.g A;Experimental source: clone Y38E10A C;Genetics: A;Gene: CESP:Y38E10A.g A;Introns: 63/2; 221/2; 261/3 C;Superfamily: Caenorhabditis elegans hypothetical protein C09E8.2
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A.Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S77556
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, September 1999 A;Reference number: Z20252 A;Accession: T26657 A;Status: preliminary; translated from GB/EMRL/DDR.
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A; Residues: 1-286 <W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-202 <KAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Start codon:
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                    126 MIIAVNAFTQQKVNVIGYSMG---SPIARKAILGGKCAENTVQLGAPLTSIIETYISVAG
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                                                                                                                                                                                                                                                          66 PVILVHGTTNSAGTFAPQAAYFRANGWSEETVYATTYGDAGVTTATNVKMLCEYVQQIRN 125
                                                                                                                                                                                                                                                                                                  36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKV--
                                                                                                                                                                                                                                                                                                                                                                    Local
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NTVCGRVSRIDGATAEKDNVPGNHDAIIANT
                                        MIVMNYLSKLDGAKNAQIHGVG-HIGLLMNS
                                                                                   ANRGTSLCDILFAPLVVPTCNTKNGLKCSSDFLTDIRSVSAYEGQYIFSIYGPSDDKVGF
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35; Conserv
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                                                                                                                                                                                                                                                                                                                                             Conservative
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26.1%;
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30.78;
                                                                                                                                                                                                                                                                                                                                           30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                    Score 149; UB -...
nrad. No. 5.7e-05;
nrad. No. -has 71;
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Pred. No. 1.5e-05;
7; Mismatches 45;
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RESULT
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ZK617.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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AE1975
                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EME
A;Experimental source:
                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-344 <WIL>
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A; Residues: 1-211 <KUR>
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                                                                                                                                                                                                                                                                                             A; Gene: CESP: ZK617.2
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Best Local :
                                                                                                                                                                                                                                                                                                                      Genetics:
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Best Local :
                                                                                                                                                                      Matches
    124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 LHSWMLKDFRSIEAVAAALAEPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 GHIGLLMN----SQVNSLIKEGLN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 QHPGCVQMRPNSLFLQDLNRDVQMLEQLNFTSIWTPYDLMIIPTHSSKMPVGKELTIPVA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 ALPG---TDPN--
                                       88 RFVQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIEN
                                                                                                                         36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 QVADYVCATITPEQPFDLVGFSMGGIVSRYYVQKLGGISRVQRFVTISSPHHGTVVAYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 KVLDE----TGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTT---SK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPV-LSRFVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ORNPYLLYHGITDTETVFNPMAVYLRQLGWTYYTLNLVP-----NNGEAPLNYLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alr1352
    RFIETVLKYTGAQKIDVIGYSMG--
                                                                                  PVVFVHGLNNEAGSLWKIARDFTNANYPRQYLFATT-WGKGTEPLNLNVAMSCTHVQHVR 123
                                                                                                                                                                                                                                                        62/2; 121/3; 288/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                       Similarity
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                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                            EMBL:Z73897; PIDN:CAA98062.1; GSPDB:GN00022; CESP:ZK617
pe: clone ZK617
                                                                                                                                                                                                                                                                                                                                          clone
                                                                                                                                                                                     13.1%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.3%;
                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                 Score 142.5; DB 2;
Pred. No. 0.00025;
9; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 145; DB 2;
Pred. No. 8.3e-05;
3; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                          from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -QKILYTSIYSSAD-MIVMNYLSKLDGAKNAQIHGV 185
SPIARKAILGGKCVDNPNVALGPSLHSRVHTYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        мау
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#text_change 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (strain PCC 7120)
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                                                                                                                                                                    Indels
                                                                                                                                                                                                         Length
                                                                                                                                                                    57;
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                                     -VVT 132
                                                                                                                                                               Gaps
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A; Title: An accessory gene, lipB, required A; Reference number: S36248; MUID:94018652; A; Accession: S36248
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C;Date: 15-Oct-1999 #sequence_revision
C;Accession: T20712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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       A; Cross-references: EMBL: X70354
                           A; Molecule type: DNA
A; Residues: 316-358 <FR2>
                                                                                                                                                                        A; Note: sequence extracted from NCBI backbone (NCBIN:121572, R; Frenken, L.G.J.; BOS, J.W.; Visser, C.; Mueller, W.; Tomma:
                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-358 <FRE>
                                                                                                                                                                                                                                                                                                                                           A; Title: Cloning of the Pseudomonas glumae lipase gene and A; Reference number: A48952; MUID:93119130; PMID:1476423 A; Accession: A48952
                                                                                                                                                                                                                                                                                                                                                                                                                R; Frenken, L.G.; Egmond, M.R.; Batenburg, A.M.; Bos, J.W.; Appl. Environ. Microbiol. 58, 3787-3791, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                             triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas glumae
C;Species: Pseudomonas glumae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A48952; S36248; S37291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 3
A; Introns: 13/2; 115/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, August 1994 A; Reference number: Z19313
                                                                                                                                                                                                                            A; Experimental source: PG1
                                                                                                                                                                                                                                               A;Cross-references: EMBL:X70354; NID:g49205; PIDN:CAA49812.1;
                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP:F10F2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:235598; PIDN:CAA84650.1; GSPDB:GN00021; CESP:F10F2.3
A;Experimental source: clone F10F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-300 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                 Frenken, L.G.J.; Bos, J.W.; Vi
ol. Microbiol. 9, 579-589, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: Caenorhabditis elegans hypothetical protein C09E8
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 LGGANRSTTSKALP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
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les 43; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAKAAEHNPVVMVHGIGGASY-----NFAGIKSYLVSQGWSRGKLYAVDFWDKTGT- 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDGNCTLGPPLGAKVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ENVVTLG---GANRST 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGDPVEKEPVIFIHGSGDTALFTQQPLATGFSRSIQYFLEQNYTEAELYATTWGDTWGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMLDTYSTIHTCGNLIYLRRFLEAVIGYTGAKKVDIIAHSVG---VPLMRKVVKGGTLIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YMACGKKASEFTGAHEWKVEGRNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208/3; 268/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.8%;
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Pred. No. 0.00
17; Mismatches
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                                                                                                     for the production PMID:8412704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50;
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                                                                                                                                                                          Tommassen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                            determination of the
                                                                                                                                                                                                                                                                                                                                                                                                                                         Visser,
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                                                                                                                           of active Pseudomonas
                                                                                                                                                                                                                                                  PID: g49206
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                                                                                                                                                                     J.; Verrips,
                                                                                                                                                                                                                                                                                                                                                                                                                                       C.; Verrips,
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R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; K. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.I. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-redual: Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
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                                                                                                                                                                                                                    C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                 B69470
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                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                   lipase homolog - Archaeoglobus fulgidus
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в69470

sulfate-reducing

arch

B.P.; Sykes

McDonald,

K.A.;

Dod is, E

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A;Gene: lipA
C;Superfamily: Pseudomonas triacylglycerol lipase
C;Keywords: carboxylic ester hydrolase; extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z19943
A; Accession: T24853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T12A7.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                   A; Introns: 105/3; 138/3;
                                                                                                                                                                                                                                                                                                  A; Map position:
                                                                                                                                                                                                                                                                                                                                                         A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-371 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Lennard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 15-Oct-1999
                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:T12A7.4
                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z73911; PIDN:CAA98139.1; GSPDB:GN00022; CESP:T12A7.4
                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                              Matches
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226
                                 124
                                                                     170
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                                                                                                                                                                          35 NPVVMVHGIGGA-----SYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGT-----NYN 81
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                                                                     CVTVFRLRKFVEAVMDYTGAKQINIISHSMGVTLARKVILGG-
                                                                                                     NGPV--LSRFVQKVLDETGAKKVDIVAHSMG-----
                                                                                                                                          DPVIFFHGNSDAALTANNFSTGWTTTVQYFLNQGYTLGHLYGTS-WGNTNTTAAVERDHD 169
                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATKVNLIGHSQGGLTSRYVA -- AVAPQLVASVTTIGTPHRGS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRSMRSRVAARAVAWALAVMPLAGAAGLTMAASPAAVAADTYAATRYPVILVHGLAGTD-
LGNKVRVILGIAGAN 240
                                 -GNKIENVVTLGGAN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFA-----GIKSYLVSQGWSRGKLYAVD---FWDKTGTNYNNGPVLSRFVQKVLDETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFANVVDYWYGIQSDLQSHG---AKVYVANLSGFQSDDGPN-GRGEQLLAYVKQVLAATG
                                                                                                                                                                                                              41;
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48; Conser
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                                                                                                                                                                                                                                                                                                                                                           clone T12A7
                                                                                                                                                                                                                                                                                   166/2; 218/1; 261/3; 318/1; 343/3
                                                                                                                                                                                                                                 12.6%;
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29.6%;
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                                                                                                                                                                                                          Score 137.5; DB 2;
Pred. No. 0.00071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 139.5;
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                                                                                                       -GANTPYYIKNLDG-----
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                                                                       YINADDGSCNIGKP 225
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A:Introns: 80/3; 123/2; 166/1; 200/2
C:Superfamily: Caenorhabditis elegans hypothetical protein C09E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Du, Z.; Graves, T.; Gibson, A.
submitted to the EML Data Library, July 1998
A;Description: The Sequence of Caenorhabditis elegans
A;Reference number: Z21322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C09E8.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE000981; GB:AE000782; NID:92689304; PIDN:AAB89488.1; PID:9264878
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A; Status: preliminary; I
A; Molecule type: DNA
A; Residues: 1-474 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: C09E8.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-292 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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Best Local Similarity
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223
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                                                                                                          131 VTLG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 SQVNSLIKEGLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 EALAESGADKVDLVGHSMGTFFLVRYVNSSPERAAKVAHLILLDGVWGVDAPEGIPTLAV 179
                                                                                                                                                                                77
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                                                                                                                                                                                                                                                    17 LSVTSLFAMQPSAKAAEHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKT 76
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SHVFSIFSTAD
                                                                                                                                                                            GTNYNNGPVLSRFVQKV-----LDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary; nucleic acid sequence not shown; translation not shown
                                  ----SIYSSAD 164
                                                                  EILGAPLTELVDTFLSVAGANYGSVLCILPVPVGTCNKKNGLHCDSEFLQDINNQHRYEG
                                                                                                                                                                                                                  LGMDASFGGKENPTEVPQNPVIIVHGITNKASRFGGTVAYLKSKGYKNSEIYGTTWGDSG 105
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                                                                                                                                          RTPVGLVDMKCNYVKQIRAMIIAVRQYTGQKVDVIGYSMG---SPLARKAILGGQCVDTR
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                                                                                                                                                                                                                                                                                          46;
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se: strain Bristol N2; clone C09E8
233
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24.1%;
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21.7%; Pred. No. 0.(
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                                                                                                    GANRSTTSKALP--
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                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                      Score 131; DB 2;
Pred. No. 0.0018;
Pred. No. 0.0018;
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                                                                                                                                                                                                                                                                                                                         Length 292;
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                                                                                                        DPNQKILYT-
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R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A97027
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C;Superfamily: Pseudomonas triacylglycerol lipase
C;Keywords: carboxylic ester hydrolase
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                                                                                                                                                                                                                                                                                                                                                A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-479 < KUR>
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C;Accession: A97027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Jorgensen, S.; Skov, K.W.; Diderichsen, J. Bacteriol. 173, 559-567, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
A39133
                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE001437; PIDN:AAK79004.1; PID:g15023939; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrolase of alpha/beta superfamily, probable membrane associated lipase [imported] C;Species: Clostridium acetobutylicum
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A; Residues: 1-364 < JOR>
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Best Local S
Matches 51
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Best Local Similarity
                                                                                   224
                                                                                                                                                                    166 LNIAKRFIVGFVCF--IPIINIFAMLYACHTAKIEYDHDLYKVITNKERVDSHVCKTKYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142
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                                                                                                                                                                                                                                                          Local Similarity 21.9
nes 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                CAC1028
LQIIKETGCEKVNIIAHSKGGLDSRYMVSKLEMGKYVASLTMMSSPHRGCKFVDIACKIP 337
                                      QKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDP 150
                                                                              LVLVHGVGFRDLKYINYWGRIPKELIRNG---ATIYYGNQEAW--
                                                                                                                         VVMVHGIGGAS---YNFAG-IKSYLVSQGWSRGKLY--AVDFWDKTGTNYNNGPVLSRFV
                                                                                                                                                                                                               MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA----EHN---
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InterPro; IPR002918; Lipase_2.
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Pfam; PF01674; Lipase_2; 1.
Hydrolase; Lipid degradation; Signal
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   SPECIES=P.glumae; MEDLINE=93119130;
                                                                         Bacteria; Proteobacteria; Burkholderia.
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                           SEQUENCE FROM N.A.,
                                                                                                       Chromobacterium viscosum
                                                                                                                     Pseudomonas
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EMBL; X70354; CAA49812.1; -
EMBL; A16323; CAA01279.1; -
EMBL; A32021; CAA02073.1; -
PIR; A40952; A48952.
PIR; S37291; S37291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed; entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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MEDLINE=94009622; PubMed=8405390;
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                                                                                                                                                                                                                                                                                                              InterPro; IPR000073; Abhydrolase.
InterPro; IPR000734; Lipase.
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COFACTOR: REQUIRES CALCIUM.
SUBGUNIT: MONOMER.
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ES=C.viscosum; STRAIN-ATCC 6918;
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MEDLINE-97184685; Pubmed-9032074;
MEDLINE-97184685; Pubmed-9032074;
Schrag J.D., Li Y., Cygler M., Lang D., Burgdorf T.,
Schmid R., Schomburg D., Rydel T.J., Oliver J.D., Str
Bunaway C.M., Larson S.B., Day J., McPherson A.;
"The open conformation of a Pseudomonas lipase.";
Structure 5:187-202(1997).
                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
MEDLINE=97184684; PubMed=9032073;
MEDKINE=97184684; PubMed=9032073;
Kim K.K., Song H.K., Shin D.H., Hwang K.Y.,
"The crystal structure of a triacylglycerol.
cepacia reveals a highly open conformation i
                                                                                                                                                                                                                                                                                                                                                                               "Cloning, sequence, and exp
cepacia: lipase production
                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91100343; PubMed-1987151;
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-DSM 3959
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIT
                                                                                                                                                                                                                                                            Structure 5:173-185(1997).
                                                                                                                                                                                                                                                                                                                                                                                                          Joergensen S., Skov K.W.,
                                                                                                                                                                                                                                                                           inhibitor
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                                                                                                                                                                                                                                                                                                                                                          Bacteriol, 173:559-567(1991).
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                                                                                                        fatty acid anion.
COFACTOR: REQUIRES CALCIUM.
COFACTOR: BELONGS TO THE
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                                     European Bioinformatics Institute.
                                                                                    SIMILARITY:
                                                                                                                                                 CATALYTIC ACTIVITY:
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                         non-profit
                                                                                                                                                                                                                                                                                                                                                                              in S., Skov K.W., Diderichsen B.;
sequence, and expression of a lipase gene from Pseudomonas
lipase production in heterologous hosts requires two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteobacteria;
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33, Last seq
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3.1.1.3) (Triacylglycerol
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H->A:
A -> V
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Pred. No. 0.
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subdivision;
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1 lipase from Pseudomonas
in the absence of a boun
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Strickland L.C.
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Matches: 40
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P15493; O07349; Q9KMU7;
01-APR-1990 (Rel. 14, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
MEDLINE-20406833, PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P. McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    Alm R.A., Manning P.A.;
"Characterization of the hlyB gene and its:
The El Tor haemolysin of Vibrio cholerae Ol
Mol. Microbiol. 4:413-425(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=El Tor O17 / Serotype O1;
MEDLINE=90286918; Pubmed=2162464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
NCBI_TaxID=666;
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STRAIN=El Tor N16961 /
                                                                                                                                                                                                                                                                           Manning P.
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                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                       STRAIN-El
                                                                                                                                                                                                                                                                                                                            IDENTIFICATION,
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IPR000734; Lipase.
IPR000379; Ser_estrs_site.
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Pred. No. 0.0024;
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PIR; S08007; SPIR; S15911;
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P25275;
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Bacteria; Proteobacteria.
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InterPro; IPR0007379; Ser_estrs_si
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              "Cloning, nucleotide
                                Fukase
                                                           SEQUENCE FROM N.A., AND SEQUENCE MEDLINE=92118328; PubMed=1368739;
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SIMILARITY: STRONG, TO
SIMILARITY: BELONGS TO
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CATALYTIC ACTIVITY: Triacylglycerol +
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Bacteria; Firmicutes;
NCBI_TaxID=2104;
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Putative esterase/lipase 2
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SIGNAL
"Complete sequence analysis of the genome of the pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
-!- SIMILARITY: BELONGS TO THE LIP3/BCHO FAMILY
                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=89,
Himmelreich R., Hilbert H.,
                                                                                                                                                                                                                                                                                                                               MPN473 OR MP368.
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PIR; JQ1227; JQ1227.
HSSP; P22088; 3LIP.
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                                                                                                       Herrmann
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PubMed=8948633;
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Pred. No. 0.0043;
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Q02510;
Q1-JUN-1994
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lipase precursor (EC 3.1.1.3) (Glycerol ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for nomentalities requires a linear normalities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                      InterPro; IPR000379; Ser_estrs_site.
TIGRFAMS; TIGR01168; YSIRK_signal; 1.
PROSITE; PS00120; LIPASE_SER; 1.
                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Hydrolase; Serine esterase; Complete proteome ACT_SITE 28 PARCE RELAY SYSTEM (BY SIMILARITY). SEQUENCE 268 AA; 30784 MW; 29D5F87E12090C9B CRC64;
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                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular analysis and expression epidermidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Farrell A.M., Foster T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000035; AAB96016.1;
                                                                                                                                                    EMBL; M95577; AAA19729.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93171870; PubMed=8436947;
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                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gen. Microbiol. 139:267-277(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted.
MISCELLANEOUS: THE EXPRESSION OF STAPHYLOCOCCUS LIPASE IS NEGATIVELY REGULATED BY BACTERIOPHAGE LYSOGENIZATION (LIPASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Triacylglycerol + H(2)0 = diacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                                                                                                A47705; A47705.
rPro; IPR000734; Lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONVERSION).
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Pro; IPR000379; Ser_estrs_site.
Pr00561; abhydrolase; 1.
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degradation;
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Zymogen;
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of the lipase of Staphylococcus
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Signal
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01-AUG-1992
01-DEC-1992
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                                                                                                                                                                                                                                   Priefert H., Hein S., Krueger N., Zeh K., Schmidt I "Identification and molecular characterization of eutrophus H16 aco operon genes involved in acetoin
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Dihydrolipoamide acetyltransferase component of acetoin cleaving
system (EC 2.3.1.12) (Acetoin dehydrogenase E2 component)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALCEU
                                   EMBL; M66060; AAA21950.
                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                               acetyldihydrolipoamide.
-!- COFACTOR: THE E2 COMPONENT CONTAINS
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE C
STRAIN-H16 / DSM 428 / ATCC 17699;
                                                                                                                                                                                                                                                                                                                                                                                                      Alcaligenes eutrophus (Ralstonia eutropha).
Bacteria; Proteobacteria; beta subdivision;
                       PIR; D42462; D42462.
                                                                                                                                                                                                                                                                                                                            MEDLINE=91286190; PubMed=2061286;
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           HSSP;
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                                                                                                                                                           PATHWAY: Acetoin catabolism.
INDUCTION: BY GROWTH ON ACETOIN.
SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
                                                                                                             European Bioinformatics Institute. There
                                                                                                                                                                                                    COFACTOR (PROBABLE).
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           P20708;
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Pred. No. 2.1;
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                        http://www.isb-sib
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the Alcaligenes
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IPR003089;

AB\_hydrolase

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P26876;
01-AUG-1992
01-APR-1993
15-JUN-2002
protein.
Biochim.
[4]
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                                                         Jaeger K.-E., Adrian F.-J.,
"Extracellular lipase from Extracellular l
                                                                                                                                          SEQUENCE FROM N.A., AND
                                                                                                                                                                                                      Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                   MEDLINE=92337414;
Chihara-Siomi M.,
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                                                                                                    MEDLINE=92247813; PubMed=1576157;
                                                                                                                           STRAIN-PAC1R
                                                                                                                                                                                                                         "Purification, molecular cloning,
                                                                                                                                                                                                                                                Chihara-Siomi M., Yoshikawa K., (
Sogabe Y., Nakatani T., Nishioka
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas
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40; Conser
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IPR000089; Biotin_lipoyl.
IPR003016; Lipoyl.
IPR000379; Ser_estrs_site.
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                                                                                                                                                                                     Biophys.
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                                                                                                                                                                                                                                                                                    PubMed=1632642;
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Last annotation update)
ecursor (EC 3.1.1.3) (Tr
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                   1120:315-321(1992).
                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                 PARTIAL
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                                                       Pseudomonas aeruginosa is an
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6; Mismatches
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9D5CE1F83E94892F CRC64;
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Pred. No. 2.
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                                                                                                                                                                                                                                                  Oshima-Hirayama
a T., Oda J.;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                         Winkler U.K. amphiphilic
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MQPSAKAAEHNPVVMVHG-----IGGASYNFAGIKSYLVSQGWSRG

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STITE TO DESCRIBE REPRESENTATION OF THE PROPERTY OF THE PROPER
                    Query Match
Best Local
    Matches
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EMBL; AB008452; BAA523128.1; -
EMBL; AX000441; CAB77076.1; -
EMBL; AE004712; AAG06250.1; -
EMBL; S25768; S25768
PIR; S24160; S24160
HSSP; P22088; 3LIP
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                                                                                                                                                    VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aeruginosa EF2.";
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                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00561;
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                                                                                                                                                                                                                                                                                       Hydrolase;
SIGNAL
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ANHYDROUS ORGANIC SOLVENTS.
- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = d
fatty acid anion.
- SUBCELLULAR LOCATION: DURING EARLY STATIONARY G
10% OF THE ENZYME MOLECULES REMAIN CELL-BOUND W
ARE RELEASED INTO THE GROWTH MEDIUM.
- HISCELLANEOUS: LIPASE OF STRAIN EF2 EXHIBITS SO
ACTIVITY, AND SHOWS A MARKED SPECIFICITY OR THE
OF TRIOLEIN.
                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000073; Abhydrolase.
InterPro; IPR000734; Lipase.
                                                                                                                                                                                                                                                                                                                                                                             nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE AB HYDROLASE
    l Similarity
32; Conser
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                                                                                                                                                                                                                                                                                                                                                                        IPR000379; Ser_estrs_site
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202
    Conservative
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                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                    abhydrolase;
                                                                                                                                                                                                                                                                                                         ; LIPASE_SER;
degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=1748875;
Jones C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=10984043;
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LYZES THE SYNTHESIS OF MACROCYCLIC
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                      8.1%;
28.8%;
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V
                                                                                                       CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
K -> Q (IN STRAIN EF2).
V -> I (IN STRAIN TE3285).
Q -> H (IN STRAIN TE3285).
I -> V (IN STRAIN TE3285).
    19;
                    Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                                         1. Signal;
                                                                                                                                                                                                                                                              LACTONIZING LIPASE
core 88; DB 1
ced. No. 2.6;
Mismatches
                                                                                       7DB14DF27BDE5619
                                                                                                                                                                                                                                                                                                       Complete
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CELL-BOUND
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    46;
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                                                                                       CRC64;
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WHILE ABOUT 9
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    Indels
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                                             311;
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n S., Yuan Y.,
K., Lim R.M.,
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MBL outstation -
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LIP_PSESP
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01-AUG-1992
01-AUG-1992
15-JUN-2002
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ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pfam; pF00561; abhydrolase; 1
proSITE; pS00120; LIPASE_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A40943; A40943.
HSSP; P22088; 3LIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 27-45 MEDLINE-92011544; PubMed-1917947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                         LVLSVTSLFA----MQPSAKAAEHNPVVMVHG-----IGGASYNFAGIKSYLVSQGWSRG
                                                                                                             QVYVTEV-SQLDTSEVRGEQLLQQVEEIVALSGQPKVNLIGHSHGGPTIRY
                                                                                                                                                  KLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPY
                                                                                                                                                                                                LAIGLASLAASPLIQASTYTQTKYPIVLAHGMLGFDNILGVDYWF-GIPSALRRDG--
                                                                                                                                                                                                                                                                                                              Similarity
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IPR000379; Ser_estrs_site
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311 AA;
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(Rel. 23, Last sequence update)
(Rel. 41, Last annotation update)
lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
                                                                                                                                                                                                                                                                                         Conservative
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                degradation;
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311
108
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                                                                                                                                                                                                                                                                                                           8.1%;
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                                                                                                                                                                                                                                                                                                           Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                           LACTONIZING LIPASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
; 27AC2F3DD3B334D1 CRC64;
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  PRT;
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415
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2.6;
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RESULT 12 Y045\_MYCPN ID Y045\_MYCPN

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15-JUL-1998
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; "A 460-kb DAN sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map."; DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., RR
Riley M., Davis N.W., Kirkpatrick H.A., Goe
                                                                                                                                                                                                                                                                                                                EcoGene; EG14056; yegM.
InterPro; IPR002215; H1
                                                                                                                                                                                                                                                                                                                                            EMBL; D90845; BAA15928.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita
                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                              Pfam; PF00529; HlyD; 1.
Hypothetical protein; Signal; Complete proteome
                                                                                                                                                                                                                                                                                                                                              EMBL; AE000297; AAC75135.1; ALT_INIT. EMBL; D90845; BAA15928.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Science 277:1453-1474(1997)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
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                           158
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                                                                                                                    248
366
                                                         306
                                                                                                                                              58 VSQGWSRGKLYAVDFWDKTGT-NYNNGPVLSRFVQKVLD-ETGAKKVDIVAHSMGGANTP 115
                          SIYSSADMIVMNYLSKL-DGAK 178
                                                                                       YYIKN-----
                                                                                                                    VVQAQKAGKPLVVEAWDRTNSKKLSEGTLLS--LDNQIDATTGTIKVKARFNNQDDALFP
AGISAGDRVVTDGIDRLTEGAK
                                                       NOFVNARMLVDTEQNAVVIPTAALQMGNEGHFVWVLNSENKVSKHLVTPGIQDSQKVVIR
                                                                                                                                                                               36;
                                                                                                                                                                                           Similarity
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415 i
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(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                              Conservative
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                                                                                                                                                                               22;
                                                                                   -LDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYT
387
                                                                                                                                                                                                                                     HYPOTHETICAL PROTEIN YEGM ; 26240DBBE0DE1A5F CRC64;
                                                                                                                                                                                           Score 87.5;
Pred. No. 4;
                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                           В
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                                                                                                                                                                               61;
                                                                                                                                                                                                           Length 415;
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                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration
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Nucleic

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BNI1_YEAST
P41832;
01-NOV-1995
01-OCT-1996
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma pneumoniae 
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR000044; Lipoprt_MG045.
Pfam; PF02030; Lipoprotein_8; 1.
PRINTS; PR09095; MYCMG045.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Lipoprotein; Membrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000011;
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                                                                                                                                                                                                                                                                                                                                            QFVFANFESYVSPLLLERAE -- AKQPMTFLTYPTNEKLINGFANNTYTVAVASSYAVSEL
                                                                                                                                                                                                                                                                                                                                                                         KFVKRRIIALVTILVLSVTSLFAMQPSAKAAEHNPVVMVHGIGGASYNFAGIKSYLVSQG
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                                                                                                                                                                                                                                                                                       QQQGHLLPID-WAKFNLKKTQNGSNQATIQNKEDAK---ELFTKEIGDISGELLNWGVPY
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Pred. No. 4.9;
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 EMBL; L31766; AAA34455.1; -
EMBL; Z71546; CAA96179.1; -
EMBL; Z71547; CAA96179.1; -
EMBL; X92494; CAA63225.1; -
SGD; S0005215; BNI1.
InterPro: IPR003104; FH2.
Pfam; PF02181; FH2; 1.
SMART; SM00498; FH2; 1.
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BNII OR SHE5 OR YNL271C OR NO646.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                                                               modified
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBUNIT: INTERACTS WITH PROFILIN AT THE FH1 DOMAIN.
-1- SIMILARITY: CONTAINS 1 GTPASE-BINDING DOMAIN (BBD).
-1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 1 (FH1) DOMAIN.
-1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 2 (FH2) DOMAIN.
-1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 3 (FH3) DOMAIN.
-1- SIMILARITY: CONTAINS 1 DRF AUTOREGULATORY DOMAIN (DAD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99187130; PubMed=10085293;
Lee L. Klee S.K. Evangelista M. Bound of mitotic spindle position formin Bnilp.";
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MEDLINE=96310631; PubMed=8740425;
Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K.,
"The sequence of a 24,152 bp segment from the lef-
XIV from Saccharomyces cerevisiae between the BNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fares H.F., Pringle J.R.;
"Synthetic lethals of CDC12.
Submitted (XXX-1995) to the
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FH1 (PRO-RICH).
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Saccharomyces
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CONFLICT
CONFLICT
                                                                                                                                                                            "Molecular cloning and nucleotide sequence of the Pseudomonas fragi.";
Biochem. Biophys. Res. Commun. 141:185-190(1986).
-!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)0 = fatty acid anion
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-IFO 12049;
MEDLINE-89078617; PubMed-3060375;
AOyama S., Yoshida N., Inouye S.;
"Cloning, sequencing and expression of the lipase Pseudomonas fragi IFO-12049 in E. coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIP_PSEFR
P08658;
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DOMAIN
EMBL; M14604; AAA25879.1;
EMBL; X14033; CAA32193.1;
PIR; A26383; A26383.
                                           the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lipase precursor (EC 3.1.1.3) (Triacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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SIMILARITY: BELON
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                                                 SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E.,
Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., L
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
       This
                            -!- PATHWAY: 3-hydroxyphenylpropionate degradation.-!- SIMILARITY: STRONG, TO B.CEPACIA AND PSEUDOMONAS BPHD.
                                                                                                                                       "The
                                                                                                                                                Gregor J., Davis
Mau B., Shao Y.;
                                                                                                                                                           Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., R Gregor J., Davis N.W., Kirkpatrick H.A., Go
                                                                                                                                                                                           STRAIN=K12 / MG1655; MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=K12 / CS520
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       SWISS-PROT entry is copyright.
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IPR000734; Lipase.
IPR000379; Ser_estrs_site
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ACT_SITE 90 90 BY SIMILARITY.

CONFLICT 158 158 E -> G (IN REF. 1 AND 2).

SEQUENCE 293 AA; 32585 MW; 4407DF7B90EA0E80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF00561; abhydrolase; 1.
PRINTS; PR00111; ABHYDROLASE.
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EMBL; U73857; AAB18073.1; ALT_INIT.
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P73372 synechocyst
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LFAMOP-SAKAAEHNPVVMVHG : :	, Lee J.K.; a lipase gene from Bacillus EMBL/GenBank/DDBJ database - 2. trs_site. W; 460397D7026A789B CRC64; Score 771.5; DB 2; Leng Pred. No. 4.6e-53; Pred. No. 4.6e-53; 1nde	.lus/Clostridium group; Bac	PRT; 215 AA. Created) Last sequence update) Last annotation update)	ALIGNMENTS	
SIGGASYNFAGIKSYL 57  :	s sp. B26."; es. gth 215; els 3; Gaps 2;	illales;			Q19310 caenorhabdi Q22420 caenorhabdi Q22420 caenorhabdi Q22451 archaeoglob Q76556 caenorhabdi Q97891 clostridium Q22d71 listeria in Q68551 pseudomonas Q56594 vibrio chol Q8xxn1 ralstonia s Q22060 caenorhabdi Q43962 acinetobact Q20437 caenorhabdi Q52614 proteus vul Q15380 caenorhabdi P72172 pseudomonas Q32y57 oryza sativ Q17622 caenorhabdi Q9huz7 pseudomonas Q9aus1 oryza sativ Q92x5 rhizobium m Q19462 caenorhabdi Q95295 rhizobium m Q19462 caenorhabdi Q9500 pseudomonas Q1376 caenorhabdi Q9500 pseudomonas Q17376 caenorhabdi Q9600 pseudomonas

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RNVLIHGVGHIGLLTSSQVKGYVKEGLNGGGQNTN 215

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Bacillus licheniformis.
Bacteria; Firmicutes; Bacillus/Cl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9K5F4
                                                                                                               Bacillus sp. BP-6, and Bacillus subtilis.
Bacteria; Firmicuttes; Bacillus/Clostridium Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel.
01-MAY-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Over-expression and properties of a purified licheniformis lipase: a comparative report on Enzyme Microb. Technol. 28:705-712(2001).

EMBL; AJ297356; CAB95850.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9K5F4;
SPECIES-Bacillus sp. Ruiz C., Pastor J., 1
                                                                                                             Bacillaceae;
                                                                                                                                                                                                       Extracellular esterase precursor LIPA OR LIPB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01674; Lipase_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nthangeni M.B., Patterton H.G., Litthauer D.;
                                                                                                                                                                                                                                                                                                                                                 P94444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002918; Lipase_2.
InterPro; IPR000379; Ser_estrs_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11339956;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1402;
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                                                                                       NCBI_TaxID=187867,
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                                               EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDPN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEHNPVVMVHGIGGASYNFAGIKSYLVSOGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AA;
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                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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  Diaz
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BP-6; STRAIN=BP-6;
Diaz P.;
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Last
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Last annotation update)
ursor (EC 3.1.1.1) (YFIP)
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annotation update)
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WSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKNL 12:

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RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Nobakk M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Noone D., O'Reilly M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Punnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rager M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Tosato V., Uchiyama S., Vandenbol M., Vanider F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Westzenerger T.,
                                                                       Matches
                                                                                                        Query Match
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MEDLINE-97128783; PubMed-8973323;
Yamamoto H., Uchiyama S., Sekiguchi J.;
"The Bacillus subtilis chromosome region near 78
"The Bacillus a new two-component system, three
                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                    InterPro; IPR002918; Lipase_2.
InterPro; IPR000379; Ser_estrs_site
Pfam; PF01674; Lipase_2; 1.
                                                                                                                                                                                                                                                                             EMBL; D78508; BAA11406.1; -. . EMBL; Z99108; CAB12664.1; -.
                                                                                                                                                                                                                                                                                                               SPECIES=B.subtilis; STRAIN=168;
Kunst F., Ogasawara N., Yoshikawa H., Danchin
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
EMBL; AJ430985; CAD24006.1; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viari A., Wambutt R., Winters P., Wipat A., Yoshida K., Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kunst F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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                                                                                                                                                                                  Hydrolase; Signal;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:249-256(1997).
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MEDLINE=98044033; Pu
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BP-6 esterases. Comparison with Bacillus subtilis and Bacillus pumi
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ilis.";
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                 VKRRIIALVTILVLSVTSLFAMQPSAKAAE--HNPVVMVHGIGGASYNFAGIKSYLVSQG
MKKVLMAFIICLSL-ILSVLAAPPSGAKAESVHNPVVLVHGISGASYNFFAIKNYLISQG
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                                                                                       Similarity
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Bertero M.G., Bessiere
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                                                                                                                                               210
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                                                                                                                                               AA;
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PubMed=9384377;
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28
210
                                                                                                                                               22363 MW;
                                                                                       67.2%;
68.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wedler E., Wedler H., Weitzenegger Yamamoto H., Yamane K., Yasumoto K.
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                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zumstein E., Yoshikawa H., Danchi
ce of the gram-positive bacterium
                                                                                       Score 731.5;
Pred. No. 6.
                                                                                                                                                                                                   proteome
                                                                                                                                                                  EXTRACELLULAR ESTERASE
                                                                                                                                                                                      POTENTIAL
                                                                                                                                               4358843F882C690A CRC64;
                                                                       Mismatches
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                                                                                         2e-50;
                                                                                                          DB 16;
                                                                                                                                                                                                                                                                                                                                     A.;
databases
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                                                                       Gaps
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Best Local S
Matches 142
                                           O9RSP6
O9RSP6;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
Deinococcus radiodurans.
Bacterla: Thermus/Deinococcus
Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
                              Lipase, putative DR2078.
                                                                                                                                                                                                                                                                                                                                                                                                            Q8RJP5;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                               Submitted (FEB-2002) to the EMBL; AJ430831; CAD23620.1;
                                                                                                                                                                                                                                                                                                                                                                 Bacillaceae; Bac
NCBI_TaxID=1404;
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                                                                                                                                                                                                                                                                                       Signal; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                      Extracellular esterase
                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC9885;
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                                                                                                                                                                                                                                                                                                                                                                                        Bacillus megaterium
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                                                                                                                      IHGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
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                                                                                                                                                                                  WSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKNL
                                                                                                                                                                                                                     VKRRIIALVTILVLSVTSLFAMQPSAKAAE--HNPVVMVHGIGGASYNFAGIKSYLVSQG
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                                                                                                                                                                         WQSNKLYAIDFYDKTGNNLNNGPQLASYVDRVLKETGAKKVDIVAHSMGGANTLYYIKYL
                                                                                                                                                                                                      MKKVLMAFIICLSL-ILSVLAAPPSGAKAESVHNPVVLVHGISGASYNFFAIKNYLISQG
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                                                                                                              LYGIGHIGLLSNSQVYGYIKKGLNGGGLNTN
                                                                                                                                                                                                                                     142;
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                   210 AA;
                                                                                                                                                                                                                                     Conservative
                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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210 E
22411 MW;
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Pred. No. 5.5
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               group;
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annotation update)
(EC 3.1.1.1).
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               Deinococci;
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Query Match
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Matches 61
SEQUENCE: STRAIN=A3(2);
STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D.,
Rinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                       Q9KY65;
01-OCT-2000
01-OCT-2000
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                                                                                                                                                                                                                 Brown S.P., Harris D.;
Submitted (MAY-2000) t
                                                                                                                                                                                                                                   Brown S.P., H
                                                                                                                                                                                                                                                                                                    Actinomycetales; Streptomycineae;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                      Putative secreted lipase. SCO4799 OR SCD63A.10C.
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Science 286:1571-1577(1999).
EMBL; AE002044; AAF11628.1;
TIGR; DR2078; -
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SEQUENCE FROM N.
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EMBL/GenBank/DDBJ databa
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Pred. No.
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ismatches 93;
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                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, Putative secreted lipase.
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InterPro; IPR000379; Ser_estrs_site.
InterPro; IPR000379; Ser_estrs_site.
PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 331 AA; 35137 MW; 3E0E7
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Nature 417:141-147(2002).
Redenbach M
Kinashi H.,
                                                                       James K.D., Parkhill Submitted (JUL-1999)
                                                                                                                                         STRAIN=A3(2);
Saunders D., Harris
Submitted (JUL-1999)
                                                                                                                                                                                                          Actinomycetales;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                     Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
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        MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapa
                                    SEQUENCE FROM N.A. STRAIN-A3(2);
                                                                                                    STRAIN-A3(2);
                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                   SEQUENCE
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Pred. No. 2.
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                                       STRAIN=MB4T / JCM11007;
MEDLINE=21992816; PubMed=11997336;
MEDLINE=21992817; PubMed=11997336;
MEDLINE=21992817; Li W., Xu Z., Xuan Z., Hu
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu
Chen Y., Xue Y., Xu Y., Lai X., Huang L., E
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis ge
Genome Res. 12:689-700(2002).
EMBL; AE013025; AMA23831.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bentley S.D., Chatter K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H., Harris D.E., Quall M.A., Kieser H., Collins M., Erown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
Transferase;
SEQUENCE 40
                                                                                                                                                                                                                                                                                                                                    Thermoanaerobacter tengcongensis.

Pacteria: Firmicutes: Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000379; Ser_estrs_site Pfam; PF01674; Lipase_2; 1. SEQUENCE 290 AA; 30496 MW; D56E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL096849; CAB50950.1;
HSSP; Q05489; 1TAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2) /
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                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                          NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                   Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                           LIPA OR TTE0555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002918; Lipase_2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159
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1. Microbiol. 21:77-96(1996).
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  403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
  Hydrolase; Complete
03 AA; 45221 MW; DC
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Pred. No. 3
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  DC31D5E86EC2CAC4
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  CRC64;
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Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha/beta
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                                                                                                                                           Y.,
                                                                                                                                                                  Yang
                                                                                                                                           ang J
Ling
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Best Local S
Matches 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes.

Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Propionibacterineae;
Propionibacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Triacylglycerol lipase precursor (EC 3.1.1.3).
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Propionibacterium acnes, a resident of produces a 33 kDa extracellular lipase
                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Signal.
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EMBL; x99255; CAA67627.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q59644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miskin J.E., Farrell A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97312013; PubMed=9168624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1747;
 161
                                      204
                                                                                                             144
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                                  AVGLDKLVDGLPEAVKDFLSTWSYDHNMEAYGQQLKGSALMQQVYRDGDTVPGIAYTVIS
                                                                                                         AQALGAFVDRVRKATGSEKVDFVGHSQGGGILPNAYIKMYGGASKVDKLIGLVAANHGTT
                                                                                                                                                                                                                    PVVMVHGIGG----ASYNFAGIKSYLVSQGWSRGKLYAV------DFWDKTGTNYNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKN-----LDGGNKIENVVTLGGANRS- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVVMVHGIGGASYNFA------GIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVL
                                                                                                                                           GPVLSRFVQKVLDETGAKKVDIVAHSMGGANTP-YYIKNLDGGNKIENVVTLGGANRSTT 141
                                                                                                                                                                               PVILIPGTGGNAFATWSFYG--PHLAHEGYC---VYTFTTNVPVGILDEGWGFTGDVRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGGGQN
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                                                                                                                                                                                                                                                                                                                                                                                   PF01674; Lipase_2; 1.
PE; PS00120; LIPASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                                                                                                                                                                      Similarity 27.1 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      IPR000734; Lipase.
IPR002918; Lipase_2.
IPR000379; Ser_estrs_site.
1674; Lipase_2; 1.
                                                                                                                                                                                                                                                                                                                                 339 AA;
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                                                                                                                                                                                                                                                                                                                             26
35995 MW;
                                                                                                                                                                                                                                                                         14.8%;
27.1%;
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                                                                      -GTDPNQK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                                                      Score 160.5; DB 2;
Pred. No. 9.6e-05;
4; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 173.5;
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                                                                                                                                                                                                                                                                                                                               60F63DF5B5DFDBD9 CRC64;
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                                                                                                                                                                                                                                                                                         Length
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P73372;
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               lipase
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ACC OCC OCC RP RAX
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01-JAN-1998
01-JAN-1998
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01-FEB-1997
01-MAR-2002
                            SEQUENCE FROM N.A.

MEDLINE=97438518; PubMed=9293006;

Sommer P., Bormann C., Goetz F.;

"Genetic and biochemical characterization of a
                                                                                                                                               Streptomyces cinnamoneus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01674; Lipase_2; 1.
Hypothetical protein; Complete
SEQUENCE 202 AA; 22429 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hihara Y., Ikeuchi M.;
Submitted (JUN-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimpo S.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=97061201; PubMed=8905231; Kaneko T., Sato S., Kotani H., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocystis sp. (strain PCC 6803). Bacteria; Cyanobacteria; Chroococcal
                                                                                                                                   Actinomycetales;
                                                                                                                                                                                   Lipase LipA precursor.
                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D90905; BAA17403.1;
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                                                                                                                  NCBI_TaxID=53446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000379; Ser_estrs_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 27-202 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                             FVQKVLDETGA--KKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRST
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                                                                                                                                                                                                                                                                                                                                                                                                                         AEFPDRHPVVLVHGIYDTRAKFATMVDFLTKGGWS---VHCLDLVPNDGS--TSLALLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKAAEHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSR
                                                                                                                                                                                                                                                                                                                                                        QVKQYIDQKFAPQQPVDLIGFSMGGLVTRYYLQRLGGGERVRRYITISAPNQGT
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              from Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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7 (TrEMBLrel. 02, Las
2 (TrEMBLrel. 20, Las
al 22.4 kDa protein (
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                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                   Streptomycineae;
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                 cinnamomeus
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63:3553-3560(1997).
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 153.5;
Pred. No. 0.00
27; Mismatches
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8758C3119B7352EF CRC64;
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                                                                                                                                   Streptomycetaceae;
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                                                                                                                                                                                                                                                                           InterPro; IPR000734; Lipase.
InterPro; IPR002918; Lipase_2.
InterPro; IPR00379; Ser_estrs_site.
Pfam; PF01674; Lipase_2; 1.
PROSITE; PS00120; LIPASE_SER; UNKNOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002918; Lipase_2.
InterPro; IPR000379; Ser_estrs_site
Pfam; PF01674; Lipase_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                           investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL110484; CAB54398.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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InterPro; IPR000734; Lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wallis J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKV-- 93
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58; Conser
                                                                                                                                                               Similarity
  -LDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLG---:: :||::::|| :| | :|| || || || ||
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                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                        LIPASE_SER; UNKNOWN_1.; 29876 MW; 0117E6F4E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 F
29213 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                  13.7%;
26.1%;
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Last annotation update)
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                                                                                                                                                        Score 149; DB 5; L
Pred. No. 0.00061;
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Pred. No. 0.0003
4; Mismatches <
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Matches 54
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01-DEC-2001
01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Alkaline lipase (EC 3.1.1.3).
uncultured organism.
unclassified; environmental samples.
uCBI_TaxID=155900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2001) to the EMBL/GenBank/DDBJ EMBL, AF421494; AALI7608.1; -
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000774; Lipase.
InterPro; IPR0002918; Lipase_2.
InterPro; IPR000379; Ser_estrs_site.
Defair. Denig 27. 1 incee_2.
                                                                         Streptomyces coelicolor.
                                                                                                 Putative lipase.
SCO1265 OR 2SCG18.
                                                                                                                                                01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                             Q9K3H5;
                                                                                                                                                                                                                                                          Q9K3H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01674; Lipase_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1
PROSITE; PS00120; LIPASE_SER; UNKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bergquist P.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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NCBI_TaxID=1902;
                          Actinomycetales;
                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PACNDHYGSELDTVKQALQQALSKSRTGMIDVMGHSMGATLAAKAILDLGIANKVRTFVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IAGAFRGLNSCGVYPYNVPTTTCGRYGLSINSPLVNSLANKRFGKYQYAIYSWVDEIVCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGGA-----
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                                                                                                                                                                                                                                                          PRELIMINARY;
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                          Streptomycineae;
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                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                        Created)
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                          Streptomycetaceae;
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Matches 55
                                      OBYXE3;
Ol-MAR-2002 (TrEMBLrel. 20, Created)
Ol-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Ol-UN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical protein Alr1352.
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Cerdeno A.M.,
Submitted (JUI
             Anabaena sp. (strain PCC Bacteria; Cyanobacteria;
                                                                                                                             Q8YX63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:41-147(2002).
EMBL; AL390188; CAB99145.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002918; Lipase_2.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF01674; Lipase_2; 1.
SEQUENCE 289 AA; 31466 MW; 03D90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seeger K., Saunders D., Sharp S., Squares R., Squares S.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
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Submitted (JUL-2000) t
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Brown S.P., H
 NCBI_TaxID-103690;
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Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                                                                                                                                                                                                                                   EH-NPVVMVHG-IGGASYNFAGIKSYLVSQGWSRGKLYAVDEWDK-----TGTNYNNG 83
                                                                                                                                                                                                DDVVTPYTSCALAKTEGCYVNNIVLQDIDPDDHTPHVSMPYNATVLNEVLK
                                                                                                                                                                                                                         DMIVMNY----LSKLDG--AKNAQIHGVG-----HIGLLMNSQV-NSLIK 201
                                                                                                                                                                                                                                                     GLMNLARQIPGAVELLEQGAVGEVVPVWPQLQHDHLFQRELADLGETTEGVRHTVIATQY
                                                                                                                                                                                                                                                                                   AL----
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                                                                                                                                                                                                                                                                                                                                       PVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTTSK 143
                                                                                                                                                                                                                                                                                                                                                                   EHPRPVVLVHGTFGNRGYTWNTAVPLLRRHG---HRVFRLDYGQHGNPLIFGLGDIKHSA 114
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Hypothetical protein; Complete proteome.

SEQUENCE 211 AA; 23718 MW; 08A8720935DA8F75 CRC64;
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EMBL; AP003585; BAB73309.1; -.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Title: Perfect score: Sequence: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq Maximum DB seq Total number of hits satisfying chosen parameters: OM nucleic - nucleic search, using sw model Database : Searched: Scoring table: Run on: length: 0 length: 2000000000 IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0 US-09-905-666A-1 639 1 atgaaatttgtaaaaagaag.....ggggccaaaatacgaattaa May 18, 2003, 04:58:28; Search time 1429 Seconds: (without alignments)
13013.781 Million cell updates/sec 2054640 seqs, 14551402878 residues GenEmbl:\* gb\_ba:\* gb\_htg:\* gb\_in:\* em\_htg\_hum:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Bacillus
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Sequence
AX418878
                                             Giver,L.J., Minshull,J.
Novel lipase genes
Patent: WO 0206457-A 8
                                      Maxygen,
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                   Location/Qualifiers
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/organism="Bacillus k
/db_xref="taxon:1455"
                                      Inc. (US)
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/db_xref="taxon:1399"
123 c 157 g
                                                                                      Firmicutes; Bacillales;
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Patent W00206457.
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Pred. No. 1.2e
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18-JUN-2002

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REFERENCE
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Maxygen, Inc. (US)
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/db_xref="GI:18697127"
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SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN"
122 c 157 g 159 t
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Minshull,J.
                                                                 GI:21523729
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98.7%;
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Pred. No. 1.2e
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WO0206457
and Vogel, K.
                     Bacillaceae;
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18-JUN-2002

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Sequence 5
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Patent: WO 0206457-A 4 24-JAN-2002;
Maxygen, Inc. (US)
Patent:
            Novel lipase
                     Giver, L.J., Minshull, J. and Vogel, K
                                             Bacteria;
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Firmicutes;
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/db_xref="taxon:1467"
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Pred. No. 1.2e-180;
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                                             Bacillales; Bacillaceae;
24-JAN-2002;
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AX418876
                 Giver,L.J., Minshull,J.
Novel lipase genes
Patent: WO 0206457-A 6
                                                              Bacillus azotoformans.
Bacillus azotoformans
Bacteria; Firmicutes; Bacillales;
          Maxygen,
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/db_xref="taxon:1397
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Patent: W
Maxygen,
                                Giver, L.J., Minshull, J. and Novel lipase genes Patent: WO 0206457-A 3 24-JF
                                                                           Bacillus megaterium. Bacillus megaterium
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Sequence 3 from Patent WO0206457
AX418873.1 GI:21523728
                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae;
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/organism="Bacillus azotoformans"
/db_xref="taxon:1454"
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/organism="Bacillus
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ORGANISM
                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                   VERSION
                                                         AUTHORS
TITLE
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Best Local Similarity
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                                                                                                             AB000617
AB000617.1 GI:2415716
AB000617.1 GI:2415716
YCCK; NatB; YCCG; YCCK; YCCG; YC
YCCB; YCCA; YCCI; YCCH; YCCG; YCCF; YCCE; YCCE; YCCE; YCCE; YCCE; YCCB; YCCB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGGACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGCGCAACCGTTTGAC
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                 Kumano, M., Tamakoshi, A. and Yamane, K.
A 32 kb nucleotide sequence from the region of the
lincomycin-resistance gene (22-25 degree) of the Bacillus subtilis
chromosome and identification of the site of the lin-2 mutation
Unpublished
                                                                                                                                                                                                                                                                                         cds
                                                                                                                                                                                                                                                                                                         Bacillus
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                                                                                               (sites)
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122 c 158 g
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genomic DNA,
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Pred. No. 1.4
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22
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YcdF; RapJ;
YccC; yccB;
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1.4e-174;
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                                                                                                                                                                                       YceF; YceE; YceD; YceC; YcdD; YcdC; YcdB; YcdA; Triacylglycerol lipase;
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FEATURES
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamane, K.
Direct Submission
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                                                                                                                                                                                                                                                                                probable repressor of lincomycin-resistance operon"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIMVFICMMVILSSMLLLPMYLQGGLVLTÄFASGLVLLPGGILNGFMSPVTGRLFDKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="homologue of class-V proteins of
pyridoxal-phosphate-dependent aminotransferase"
                                                                                                                                                                                                                                                                                                                                                                       complement(3225.
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                                                                                                                                                                                                                                                                                                                                                                                                                  complement(3225. .3791)
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                                                                                                                                                                                                                                                                                                                                                   /gene="yccB"
                                                                                                                                                                                                                                                                                                                                                                                           /gene="yccB"
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precursor"
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/gene="y
6592, .7
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Staphylococcus aureus"
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                                                                                                                                 complement(8677.
                                                                                                                                                         NILENALDSAAEAREKAEIKLETSLRSGLYVLTCENSTPGMDPKVLDTIYQSFGRSTK
NGAHEGMGTYIIQKLVKGAFGRLDFTYRHPIFRLEIKIPFQK"
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PAVIDIWKTFCEKKSPVIRKPEAFAAAVEYYVNAISLNGASVSQAKLAKKYGVSASTI
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/gene="lipA"
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                                                                                                                                                                                                                                                                                        translation="MITLFQCLYLILFSFICYQGAAAFSHSTAASWLAAALGAAAAGL/
                                                                                                                                                                                                                                                                                                                                                                                            transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="yccE"
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/db_xref="GI:2415720"
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                                                                                                               CTGGACGGCGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGCGAACCGTTCGACG 420
                                                                                                                                                                                                       AAAGTGGATATTGTCGCTCACAGTATGGGTGGCGCGAACACACCTTACTACATAAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGCTGTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTT 120
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                                                                                                                                                                                                                                                                       AACAATGGACCGGTATTATCACGATTTGTGCAAAAGGTTTTAGATGAAACGGGTGCGAAA
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                                                                                                                                                                                                                                                                                                                                                            GGCTGGTCGCGGGACAAGCTGTATGCAGTTGATTTTTGGGACAAGACAGGCACAAATTAT
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                                                                                       CTGGACGGCGGAAATAAAGTTGCAAACGTCGTGACGCTTGGCCGCGCGAACCGTTTGACG
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/TTMLRMIASLLEPSQGVITVDGFDTVKQPAEVKQRIGVLFGGETGLYDRMTAKENLQY
FGRLYGLNRHEIKARIEDLSKRFGMRDYMNRRVGGFSKGMRQKVAIARALIHDPDIIL
FDEPTTGLDITSSNIFREFIQQLKREGKTILFSSHIMEEVQALCDSVIMIHSGEVIYR
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9522. .10262
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/db_xref="G1:2415725"
/db_xref="G1:2415725"
/tcanslation="mykyglyddyrydlekleaivsrmodveivfstdsakeayrrvk
NGDIDLLLADIEMPHMSGYELADLIKSHSLDVDVIFVTGHGGYAVHAFDLNVHDYIMK
PYYADRLAASFDRYLKKKTETSLNGRILIKQKSEMHYLQKKDIIFAERTGRSTTIVTT
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/transl_table=11
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/gene="natB"
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/db_xref="GI:2415727"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="function of NatB is not known, Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAA22236.1"
/db_xref="GI:2415726"
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/transl_table=11
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Pred. No. 3.8e-164;
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/organism="Bacillus subtilis" /strain="168"

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REFERENCE
AUTHORS
      FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Azevedo, V. Bertero, M.G. Bessleres, P., Bolotin, A., Brignell, S.C., Brorriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Brorriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Brorriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Brorriss, R., Boursier, L., Candwell, B., Capuano, V., Choi, S. K., Codani, J.J., Connerton, I.F., Cummings, N.J., Carter, N.M., Choi, S. K., Codani, J.J., Connerton, I.F., Cummings, N.J., Carter, N.M., Choi, S. K., Codani, J.J., Connerton, I.F., Cummings, N.J., Carter, N.M., Choi, S. K., Codani, J.J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, W., Fujita, W., Fujita, W., Fujita, W., Fujita, W., Galizzi, A., Galizzi, A., Galizri, A., Wallado, A., Galizri, A., Wallado, A., Galizri, A., Wallado, A., Galizri, A., Wallado, A., Liu, H., Manbutt, R., Jazarevic, V., Lee, S.M., Levine, A., Liu, H., Manbutt, R., Galizri, T., Takahashi, Y., Sato, T., Sekowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Sorokin, A., Tanakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Viari, A., Wallado, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H. and Danchin, A., Handa, H.F., Zumstein, E., Yoshikawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCAGTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGTGCTAAAAAACGCT
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                            Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteu Regulation de l'Expression Genetique, 28 rue du Docteur Roux, Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 68 89 48
                                                                                                                                                                                                               2 (bases 1 to 221160)
Kunst, F., Ogasawara, N.,
                                                                                                                                                                                      Direct Submission
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299105.1 GI:26
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Kunst, F., Ogasawara, N.
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Location/Qualifiers
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                                                                                                                                                                                                                                                            FIDGVSLDLSKINKDSDIEADIPLPDGVĶKISPSKVTLHIEVDSEADQKFENVPIKTV
GLSSSQNIEFLDPESQAIDVTAKGSPTNINKLKKSDIELYVNVSDLEDGEHSVKLEVN
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2366. .
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1552. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MEMMIKKRIKQVKKGDQDAFADIVDIYKDKIYQLCYRMLGNVHE
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IIVSEETGGVSVAKNGDLHRELTEEALKEMLEAEFKKNTRDTSSNRWYWRGRKNG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVIVLVRMASQYLGLSTLQWLMDQAITWGFLAIIIIFQPELRRALEQLGRGRFFSRSG
TPVEEAQQKTIEAITKAINYMAKRRIGALLTIERDTGMGDYIETGIPLNAKVSSELLI
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similar to hypothetical proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNGEKYMASAGQVTGQIEEINQLFDWTWYKMKSAGKSVLDAFNPNGEE'
                                                                                                                                                                                                                                                                                                                                                                       VEPSVIKITVPVTSPSKKVPFKIERTGSLPDGVSIANIESSPSEVTVYGSQDVLDSLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="GI:2632459"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB11967.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="GI:2632458"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'codon_start=1
'transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="sigW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "ybbp"
. 2373
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.2373
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                                                                                                                                                                 " Tdd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECF-type sigma factor (sigma-W)"
                                               Query Match
Best Local Similarity
              Matches
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                  598;
              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(7883. .8794)
/gene="alkA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(7883. .8794)
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                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SWISS-PROT:P37878"
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7462. .7602
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                  Mismatches
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VSVVPLQLIAYYAALHRGCDVDKPRNLAKSVTVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="L-glutamine-D-fructose-6-phosphate
amidotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDTVVSTVMSNLGFYKALEKEGIKSVQTAVGDRYVVEAMKKDGYNVGGEQSGHLIFLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSKKPLFIFLSQSGETADSRAVLVQVKALGHKALTITNVPGSTLSREADYTLLLHAGP
EIAVASTKAYTAQIAVLAVLASVAADKNGINIGFDLVKELGIAANAMEALCDQKDEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSVPGDIAAAVAEADRIYIIGCGTSYHAGLVGKQYIEMWANVPVEVHVASEFSYNMPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDNDNRETIFVAKNKSPLLVGLGDTFNVVASDAMAMLQVTNEYVELMDKEMVIVTDDQ
VVIKNLDGDVITRASYIAELDASDIEKGTYPHYMLKETDEQPVVMRKIIQTYQDENGK
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ENYVQLKQEYLQDVELKSDTDTEVVVQVIEQFVNGGLETEEAFRKTLTLLKGSYAIAL
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IGRDTRISGHMLEGALVAGLLSIGAEVMRLGVISTPGVSYLTKAMDAEAGVMISASHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'function="adaptative response to DNA alkylation"
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Dartois, V., Baulard, A., Schanck, K. and Colson, C.
                                                                                                                                                                 M74010.1 GI:143153
lipA gene; lipase
Bacillus subtilis (strain
Bacillus subtilis
                                                                                           Biochim. Biophys.
92329538
1320940
                                                                                                            Cloning, nucleotide sequence and expression in a lipase gene from Bacillus subtilis 168 Biochim. Biophys. Acta 1131 (3), 253-260 (1992)
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   /gene="lipA"
414. .419
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                  CAAATTCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATT
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                                                                                                                       ACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTAC
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Vandamme, E., Schanck-Brodrueck, K.H., Colson, C. and Hanotier, DNA segment coding for a specific lipase, vectors for the expression thereof, microorganisms transformed by these vectouse of these microorgenisms for the production of the lipase Patent: EP 0243338-A 1 28-OCT-1987;
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SSADMIVMNYLSRLDGARNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGQNTN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           artificial sequences.
1 (bases 1 to 1831)
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/db_xref="taxon:32630"
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            CTGGACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGCGCAACCGTTCGACG
                                AACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAA
                                                                                                                                       GGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTAT
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                                                                              AACAATGGACCGGTATTATCGCGATTTGTGCAAAAGGTTTTAGATGAAACGGGTGCGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                     artificial sequences.

1 (bases 1 to 1831)

Vandamme,E., Schanck Brodrueck,K.H., Colson,C. and Hanotier,J.D.V.

DNA segment coding for a specific lipase, vectors for the
expression thereof, microorganisms transformed by these vectors and
use of these microorgenisms for the production of the lipase
Patent: EP 024338-A 4 28-OCT-1987;

FINA RESEARCH 5.A.
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92.8%;
Score 565.4;
Pred. No. 6.2e
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## ALIGNMENTS

Bacillus lipase polynucleotide #1.

08-MAY-2002 ABK33819;

(first entry)

ABK33819 standard; DNA;

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BP.

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Giver LJ,
                                                    13-JUL-2000;
21-JUN-2001;
                                                                                                                                                                               human foodstuff; cheese; food emulsifier; leather tanning; gene; ds; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
                                                                                    13-JUL-2001; 2001WO-US22160
                                                                                                         24-JAN-2002
                                                                                                                             WO200206457-A2
                                                                                                                                                  Bacillus pumilus.
                                                                                                                                                                       gastrointestinal
                              (MAXY-) MAXYGEN INC
                                                                                                                                                                                                                           Lipase; Bacillus; animal feed;
           Minshull J,
                                                  2000US-217954P
2001US-300378P
           Vogel K;
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                                                                               CAAATTCATGGCGTTGGGCACATTGGTTATTGATGAACAGCCAAGTCAACAGCCTGATT
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al feeds, as agents of flavour modification and
disease and coeliac disease
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RRESULT 2
ABK33825
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AX ABK33825
AX ABK33825
AX ABK33
XX BAC1
DE BAC1
XX Lipa
KW Lipa
KW Cosel
KW Gast
KW Gast
KW Gast
KW Gast
XX BAC1
XX W20
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PP 13-J
PP 21-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipase; Bacillus; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; gene; ds; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 81;
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21-JUN-2001;
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animal feeds, as agents of flavour modification and for treating
ohn's disease and coeliac disease -
CACGGTATCGGAGGAGCTTCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCAG
                                                                                                                               TCGCTGTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTT
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DB; AAU83847.
                                                                                                      TCGCTGTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTT
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2001US-300378P
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Pred. No. 4.3e-187;
0; Mismatches 6;
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      Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
                                                                                                 (MAXY-) MAXYGEN INC
                                                                                                                     13-JUL-2000;
21-JUN-2001;
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DB; AAU83848.
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2001US-300378P
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RESULT 4
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Local Similarity 98.9%;
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                                                                                                                                                              CTGGACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGCGAACCGTTCGACG
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AAAGAAGGACTGAACGGCGGAGGCCACAATACAAATTAA
                                                     CAAATTCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATT
                                                                                                          AGCAGTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGTGCTAAAAAACGTT
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21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal lipid related condition; antiinflammatory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leather processing;
coeliac disease; inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cleic acids encoding lipase enzymes which are useful animal feeds, as agents of flavour modification and ohn's disease and coeliac disease -
AACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAA
                                                          GGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTAT
                                                                                                                 CACGGTATCGGAGGAGCTTCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCAG
                                                                                                 CACGGTATCGGAGGAGCTTCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCAG
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                                          GGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTAT
                                                                                                                                                            TCGCTGTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTT
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631; Conserv
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2001US-300378P.
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98.7%;
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                                                                                                                                                                                                                                                                              Score 626.2; DB 24
Pred. No. 4.3e-186;
0; Mismatches 8;
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RESULT 5
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                                                                                                Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
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21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                              Bacillus circulans
                                                                                                                                                                                                                                                                                                                                                                                        gastrointestinal
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DB; AAU83845.
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2001US-300378P.
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The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning.

in in Claim 81;

Page 118-119; 196pp; English.

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RESULT 6
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AC ABA9
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Best Local S
Matches 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase polynucleotides of the invention.
 autoimmune
gene; ds.
                       Lipase 396;
                                               Bacillus
                                                                      16-APR-2002
                                                                                               ABA96150;
                                                                                                                      ABA96150
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                                              circulans lipase
                                                                                                                    standard;
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           ; spore protein application; immune response; HIV; cancer; disorder; inflammatory; allergic reaction; autoantigen:
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                                                                     entry]
          inflammatory; allergic
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Pred. No. 4.3e-186;
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          reaction; autoantigen;
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Best Local S
Matches 631
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having
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Pred. No. 4.3e-186;
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The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipase; Bacillus; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; gene; ds; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
                                                                                                                                                                                               Claim 81; Page 119; 196pp; English.
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21-JUN-2001;
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Matches 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tranning/processing of leather and as cleaning agents. They are also useful for treating Crohm's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences ABR33819-ABR33874 represent Bacillus lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
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21-JUN-2001; 2001US-300378P.
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           GACAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAGATTTATATACACATCCATTTA
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GACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTA
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Pred. No. 7e-180;
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                                                                                                                                                                                                                                                                                                                                                                                 The DNA sequence encodes recombinant lipase which has the activity of the known lipase obtd. by culturing Geotrichum candidum and is suitable for similar industrial uses e.g. oleic acid esterification as a flavouring agent and in the processing of unsaturated fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Production of lipase catalysing triglyceride(s) hydrolysis - using recombinant DNA procedures to give DNA segment coding : lipase, cloning vectors and yeast or bacterium transformants
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                                                                                                                                                                                                                                                                                                                   Sequence 1831 BP;
                                                                                                                                                                                                                                                                                                                                                            acid-contg. oils
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CACGGTATCGGAGGAGCTTCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCAG
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                                                                                                                               TCAAATTCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGAT
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Crohn's disease and

coeliac disease

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Nucleic acids encoding lipase in animal feeds, as agents of
                                                                               P-PSDB; AAU83842
                                                                                                                                                                                                                                                                  13-JUL-2000;
21-JUN-2001;
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enzymes which are useful flavour modification and
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as supplements for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase polynucleotides of the invention.
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                                                         CAAATTCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATT
                                                                                                                                   AGCAGTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGTGCTAAAAAACGCT
                                                                                                                                                                                           ACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTAC
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Pred. No. 1.
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1.1e-166;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipase; Bacillus; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; gene; ds; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
                                                                                                                                                                                                                                                                                                                                                 method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding lipase enzymes which are useful as supplements in animal feeds, as agents of flavour modification and for treating Crohn's disease and coellac disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 81; Page 120; 196pp; English.
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21-JUN-2001;
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              GGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTAT
                                                                             CACGGTATCGGAGGAGCTTCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCÄG
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                                                                                                                                            TCGCTGTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTT 120
 GGCTGGTCGCGGGACAAGCTGTATGCAGTTGATTTCAAGGACAAGACAGGCACAAATTAT
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2001US-300378P
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92.5%;
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Pred. No. 5.2e
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21-JUN-2001;
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DB; AAU83864.
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The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements animal feeds, as agents of flavour modification and fat modification in

ä in Claim

81; Page 127; 196pp; English

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RESULT 13
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AC ABK33
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DT 08-MP
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DE Bacil
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KW Lipas
KW humar
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Lipase; Bacillus; animal recu; recording fleather tanning; gene; ds; human foodstuff; cheese; food emulsifier; leather tanning; gene; ds; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory
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531; Conser
                                                                                                     lipase polynucleotide #53
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Mismatches
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8.2e-154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease.
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21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 544 BP; 172 A; 102 C; 138 G;
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531; Conserv
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2001US-300378P.
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420 515 455

300 395 240 335

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                                                                                                                                                   The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigastion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase
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                                                                              Sequence 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 81;
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21-JUN-2001;
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2001US-300378P.
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  81.
97.
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.2; DB 24;
8.2e-154;
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                         Length
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                                                                                                                                   Synthetic
                                                                                                                                                                                                                                         Bacillus
                               13-JUL-2000;
21-JUN-2001;
                                                                 13-JUL-2001;
                                                                                        24-JAN-2002
                                                                                                             WO200206457-A2
                                                                                                                                                           gastrointestinal
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2001US-300378P.
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Best Local Similarity
Matches 530; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding lipase enzymes which are useful as supplements in animal feeds, as agents of flavour modification and for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1.
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Gapop 10.0 , Gapext 1.0
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639
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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S-09-280-116-70
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529, Appl
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US-07-930-678-1
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APPLICANT:
APPLICANT:
                                                                                                                                      TELEFAX:
                TOPOLOGY:
                                                                                                                                                                                                                                 NAME:
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                                                                 LENGTH:
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28.4	28.4	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	29	29	29	29.2	29.2	29.2	29.4
4.4	4.4	4.5	4.5	4.5	5	5	4.5	5	4.5	4.5	<b>4</b> .5	4.5	5	4.6	4.6	4.6	4.6
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Sequence 9, Appli	Sequence 9, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 73, Appl	Sequence 65, Appl		Sequence 1, Appli	Sequence 1, Appli	Sequence 1248, Ap	Sequence 1, Appli	Sequence 9, Appli	Sequence 320, App	Sequence 4, Appli	Sequence 5, Appli	Sequence 33, Appl	Sequence 4, Appli

## ALIGNMENTS

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Sequence 1, Application US/07930678 Patent No. 5427936
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                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/EP91/00
FILLING DATE: 08-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 12
FILLING DATE: 14-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1992101:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                          TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: TITLE OF INVENTION:
 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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CITY: Alexandria
                                   STRANDEDNESS:
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                               NUCLEIC ACID
DEDNESS: double
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1800 Diagonal Road,
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WILKE, Detlef
FOULLOIS, Birgit
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                                                                                Sequence 14,
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Best Local Similarity
                                                                    GENERAL INFORMATION:
             APPLICANT: SCHEIFL APPLICANT: FALKNER TIȚLE OF INVENTION:
                                                        APPLICANT: DORNER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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LOCATION:
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SEQUENCES:
                          FALKNER,
                            SCHEIFLINGER, F. FALKNER, F. G.
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             RECOMBINANT FOWLPOX VIRUS
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Pred. No. 7.8
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
 1081
                                                              1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,766
REFERENCE/POCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                              625 CAAAATACGAA 635
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CITY: Alexandria
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TOPOLOGY: 11
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/232,463
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ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: APPLICATION NUMBER:
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 RRRRRRRRRR 1071
                                                                                         GGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGGGGGC 624
                                                              AATTACTTATCAAAATTAGACGGTGCTAAAAACGCTCAAATTCATGGCGTTGGGCACATT 564
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: LOCATION: (1)..(502)
: OTHER INFORMATION: n = a,
US-09-280-116-70
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Best Local
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TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JI., Gerald M.
REGISTRATION NUMBER: 20.977
REFERENCE/DOCKET NUMBER: 20.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
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ORGANISM: Homo sapiens
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                  COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BIRCH, ST
STREET: P.O. BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
                                                                                                                                            APPLICATION: NUMBER: US/0
FILING DATE: 26-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 CACTTGTAACAATTTTGGTGCTGTCAGTCAGTCGCTGTTTGCGATGCAGCAGCCGTCAGCAA 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGTGGGAA 209
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                                                                                                                                                                US/08/978,589£
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                                                           20-4336P
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Pred. No. 0.024;
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; TYPE: DNA
; ORGANIZM: E. coli JM 109/pal 612 strain
US-09-336-601-2
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US-09-336-601-2
                                                                           US-09-466-257A-7
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                                GENERAL INFORMATION:
                                            Sequence 7, Application US/09466257A Patent No. 6337190
                                                                                                                                                                                                                                                                          Query Match
Best Local
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CURRENT FILING DATE: 1999-06-21
EARLIER APPLICATION NUMBER: 09/034,007
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 2
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 2185-349P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MITSUDA, Satoshi
TITLE OF INVENTION: PRODUCTION OF OPTICALLY ACTIVE SPHINGOID COMPOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SUGAI, Takeshi
APPLICANT: ISHII, Takeshi
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                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn
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LOCATION:
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                                                                                                                                        GAATCTGATCGGCCATAGCCAGGGCGGCCTGACATCGCGTTA 416
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5. 6184008
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Hwang, Tzann-Shun
Wu, Szu-Pei
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Pred. No. 0.
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APPLICANT:

Chou, Hsin-Hua Chen, Hwa-Yi Lin, Lung-Shen

APPLICANT:

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; ORGANISM: Bacillus sphaericus
US-09-466-257A-7
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                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 67; Conserv
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CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LECTURE 1114
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Best Local Similarity 53.6%;
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 9
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TITLE OF INVENTION: A No. 6337190el D-Amino Acid Aminotransferase For
TITLE OF INVENTION: Simultaneously Producing
TITLE OF INVENTION: Glutaryl-7-Aminocephalosporanic Acid And D-Amino Acid
FILE REFERENCE: 1476-4003
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TITLE OF INVENTION: A No. 6337190el D-Amino Acid Aminotransferase For
TITLE OF INVENTION: Simultaneously Producing
TITLE OF INVENTION: Glutaryl-7-Aminocephalosporanic Acid And D-Amino Acid
FILE REFERENCE: 1476-4003
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE:
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545 TTCAT 549
                                                        648 GTGGAGATATTATCACAGAATGTTCTTCTGCTAATGTCTATGGTATTAAAGATGGTAAAC
                                                                            485 GTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGTGCTAAAAACGCTCAAA 544
                                                                                                                                  588 GCGCGGTACTTGCGAAACAAGAAGCATCTGAAAAAGGTTGTTACGAAGCCATTTTACACC 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPPLICATION NUMBER: US/09/466,257A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hwang, Tzann-Shun
Wu, Szu-Pei
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Lin, Lung-Shen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chou, Hsin-Hua
                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                             Score 32.2; DB Pred. No. 0.8; 0; Mismatches
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Pred. No. 0.8;
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US-08-723-896-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-723-896-2
                                                                                         Sequence 2, Application US/08424797A Patent No. 6358714 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08723896 Patent No. 5728555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-758-2982
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
        APPLICANT: Fothering
APPLICANT: Taylor, P
APPLICANT: Yoshida,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rel CURRENT APPLICATION DATA
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LOCATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                         Fotheringham,
                                        Yoshida,
                                                          Taylor, Paul P.
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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SYSTEM: PC-DOS/MS-DOS
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                           Materials and Methods for the
Production of D-phenylalanine 19
                                          Roberta K.
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                                                                     SEQ ID NO 529
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               Sequence 529, Application US/09134001C Patent No. 6380370
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ORGANISM: Staphylococcus epidermidis -09-134-001C-529
                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                        PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                    APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                  TYPE: DNA
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NFORMATION FOR SEQ ID NO:
                                                    LENGTH: 954
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OPERATING SYSTEM: PC-DOS/MS-DOS
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EDNESS: single
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cker Drive, 6300 Sears Tower
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                                                                                                                                                                                                                                                                          RESULT 12
US-08-961-527-258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                          Sequence 258, Patent No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09798096 Patent No. 6399378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                       21854 AACCACCAAGAACAGAATCATGAAGAAAACAGAAAATCTGAACAGACCTATAACTAGTAAGG 21913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21734 ACAAGGGGACATTATAACTGATTTACAGAAGTAAAAAAGATTTATAAGAGAATATTGTGAG
                                                                                                                                                                                                                                                                                                                                        21914 AGATTGAGTTAGTAATCAGGTATCACCCAACAAAGAAAAGCTC 21956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5/
COMPUTER: HP Vectra 486/33
                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                             APPLICANT:
                                                                                             STREET: 94...
OTTY: Rockville
                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                    346 TACTACATAAAAATCTGGACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGC
                                                                                                                                                                                                                                                                                                                                                                       406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 ACAGGGACGAATTATAACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      515 CAAAATTAGACGGTGCTAAAAAC 537
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nes 103; Conserv
                                                                              COUNTRY:
                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAACGGGTGCGAAAAAAGTGGGATATTGTCGCTCACAGTATGGGTGGCGCGCAACACACCT
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                                                                                                                                                                                                                                                                                                                                                                      GCGAACCGTTCGACGACAAGCAAGGCGCTTCCGGGAACAGATC 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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6420135
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                                                                 20850
                                                                                                                          9410 Key West Avenue
                                                                                                                                                                                                          Charles Kunsch
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                                                                                                                                            Human Genome Sciences,
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89
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 MSDOS
                                                                                                                                                                                         Streptococcus pneumoniae
                                                                                                                                                                               195
                               3.50 inch, 1.4Mb storage
version 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31.8; DB 4;
Pred. No. 0.96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 99500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECQL2 EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120; Indels
                                                                                                                                                                                           Polynucleotides and
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SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US

US/08/961,527

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION:

FILING DATE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Apr-
No. 577324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.8%;
Best Local Similarity 48.8%;
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 15-MAY-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1431
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1371 GGAACGAGTTTTGAACAAGTAGATAGGGTTGTTTCCGAAAATCCAGCAGATACTTTACTT 1430
                                                     ATTORNEY/AGENT INFORMATION:
                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
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                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                          COUNTRY: UZIP: 11530
                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGCTTCCGGGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACAGCAGTGCC 489
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                                                                                                                                                                                                                                                                                                       Garden City
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                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                Robinson,
                                                                                                                                                                                                                                                                                                                                                                                                                               Wittrup, Dr. Karl D.
                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                        SCULLY,
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                           NUMBER:
                                                                       06-JUL-1993
                                                                                                                                  15-MAY-1995
'MBER: 31,346
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                                                                                                                                                                                                                                                                                                                                                                                   RECOMBINANTLY EXPRESSED PROTEINS
                                                                                                                                                                                                                                                                                                                                      SCOTT, MURPHY & PRESSER
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                                                                                                                                                 US/08/441,139
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Pred. No. 2.8;
0; Mismatches
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324 TATGGGTGGCGCGAACACCCTTACTACATAAAAAATCTGGACGGCGGAAATAAAATTGA 38:

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В
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                                                                                                                                   ; FEATURE:

NAME/KEY: misc_feature

: LOCATION: (1)...(289)

: OTHER INFORMATION: n = A,T,C or G

US-09-007-005-17
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                                                                                                                                                                                                                                                  SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 6030 base pairs
                                                                    Matches
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                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5572 TCAACAGCGAACACAAAA 5589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5452 AAAAGTTTTCTGAAATACAAATTAACAGCTTTATATCCCAGCTGATTACTTCCCCAGTAA 5511
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TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                              264 ATTTGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAG 323
27
                                                                  Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 4.88;
Local Similarity 51.48;
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62585:
าา. 62585:
RURURURARCRARARURURARCRARARURGRNRNRSRNRNRSRNRNRSRNRNRSRNRNRS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roberts, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Szostak,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09007005B
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                              2.6%;
                                                                                                    4.8%;
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                                                                85; Mismatches
                                                                              Score 30.4;
Pred. No. 1.5;
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                                                                                                DB 4;
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CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EEARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
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LOCATION: (1)...(289)

OTHER INFORMATION: n = A,T,C or G

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Search completed: May 18, 2003, 07:51:45 Job time: 92 secs
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US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.8%;
Best Local Similarity 2.6%;
Matches 5; Conservative 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
                                                                                                                                                                                                                                                                                                                                                              264 ATTTGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAG 323
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2: //ggn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

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4.6	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8
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us-09-991-936-476	US-10-067-514-1	US-09-764-891-8240	US-09-938-842A-1436	US-10-123-155-412	US-08-781-986A-127	US-09-864-761-8107	US-08-781-986A-3578	US-09-783-590-8898	US-10-105-877-4	US-09-811-469-3	US-09-983-802-149	US-10-026-188-3	US-09-764-847-1876	US-10-092-154-1876	US-10-123-155-10	US-09-991-936-1676	US-09-867-701-1711	US-09-954-531-382	US-09-912-020-221	US-09-770-445-100	US-09-918-995-36871	US-09-938-842A-3864	US-09-878-766A-19	US-09-878-781-11	US-09-770-149-76
Sequence 476, App	Sequence 1, Appli	Sequence 8240, Ap	Sequence 1436, Ap	412,	Sequence 127, App	Sequence 8107, Ap	Sequence 3578, Ap	Sequence 8898, Ap	Sequence 4, Appli	Sequence 3, Appli	Sequence 149, App	Sequence 3, Appli	Sequence 1876, Ap	Sequence 1876, Ap	Sequence 10, Appl	Sequence 1676, Ap	Sequence 1711, Ap	Sequence 382, App	221,	Sequence 100, App	Sequence 36871, A	Sequence 3864, Ap	e 19	<u>;</u>	Sequence 76, Appl

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## ALIGNMENTS

RESULT 1 US-10-028-247-3

GENERAL INFORMATION:

Sequence 3, Application US/10028247 Patent No. US20020150594A1

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; LCCATION: (1)...(639)
; OTHER INFORMATION: lipase 396
US-10-028-247-3
                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 639
TYPE: DNA
                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                       Matches 631;
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/028,247
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US/60/214.161
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 09/892,208
PRIOR FILING DATE: 2001-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Methods and Compositions for Developing Spore Display TITLE OF INVENTION: Systems for Medicinal and Industrial Applications FILE REFERENCE: 18097A-033520US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Goldman, Stanley
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                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                 ORGANISM: Bacillus circulans
                                                                                                                                                                                                                                                                                FEATURE:
61
                61 TCGCTGTTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTT 120
                                                                                    TCGCTGTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTT
                                                                   Maxygen,
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Longchamp, Pascal F.
Whalen, Robert G.
                                                                                                                                       Conservative
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98.7%;
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Pred. No. 9.3e-187;
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                                                                                                                                                                12; Length 639;
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                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                        SEQ ID NO 9
LENGTH: 1011
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Publication No. US20030082781A1
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/878,781
CURRENT FILLING DATE: 2002-09-10
NUMBER OF SEO ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Potter, Andrew A. TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST TITLE OF INVENTION: STREPTOCOCCUS INFECTION FILE REFERENCE: 9000-0055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bolton, Alexandra J. APPLICANT: Perez-Casal, Jose
                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Streptococcus parauberis
                                                                                                                                                                                                                                                                     FEATURE:
327 GGGTGGCGCGAACACCACCTTACTACATAAAAAATCTGGACGGCGGAAATAAAATTGAAAA 386
                                                        315 TGCTGAAAAACATTTACATGAAAAATGGTGCTAAAAAAGTTGTTATCACTGCTCCTGGTGG 374
                                                                          267 TGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGTAT 326
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                                                                                                                                                  y Match 6.0%;
Local Similarity 56.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fontaine, Michael
                                                                                                                                    Conservative
                                                                                                                                    0;
                                                                                                                                                    Score 38.2; DB 9; Length 1011; Pred. No. 0.13;
                                                                                                                                    Mismatches
                                                                                                                                  53;
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RESULT 4
US-08-781-986A-4008
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; LOCATION: (1)..(1011)
US-09-878-766A-17
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CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                Sequence 4008, Application US/08781986A Publication No. US20030054436A1 GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION FILE REFERENCE: 9000-0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Potter, Andrew A. APPLICANT: Perez-Casal, Jos APPLICANT: Fontaine, Michae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 10
TYPE: DNA
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                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                            SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 AGT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 TGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGTAT 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 TGCTGAAAAACATTTACATGAAAATGGTGCTAAAAAAGTTGTTATCACTGCTCCTGGTGG 374
                                     APPLICATION NUMBER: US/08/781,986A FILING DATE:
                                                                                                              COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS ve
                                                                                                                                                                                                                                                  STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                STATE: Maryland
                                                                                                                                                                                                                                                                                       ADDRESSEE:
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Similarity 56.9%;
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                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                Charles Kunsch
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                                                                                                                                                       3.50 inch, 1.4Mb
                                                                                                                    version
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Pred. No. 0.13;
0; Mismatches 53;
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ATTORNEY/AGENT INFORMATION:

Benson,

APPLICATION NUMBER:

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Best Local Similarity 53.8%;
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-851
                                                  NFORMATION FOR SEQ ID NO: 4:
                                                                               REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphy
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                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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STREET: >*--
CTTY: Rockville
''nrvland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   567 TTTATTGATGAACAGCCAAGTCA 589
                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 TACAAACCACAAAAAGCTCTAAAACATTAGTTTAAACCAATGCTTAGAGCTTTCTAATTAT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                  NAME: Benson, Bob
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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                  ENGTH:
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: 13321 base pairs
nucleic acid
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                                                                  (301) 309-8512
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6/33
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RESULT 7 US-09-938-842A-3605/c

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

Sequence 3605, Application US/09938842A Patent No. US20020160378A1

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Best Local Similarity
Watches 77; Conserv:
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US-09-991-936-852/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication No.
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/128,704 PRIOR FILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/09/543,668 PRIOR FILING DATE: 2000-04-07.
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/991,936
CURRENT FILING DATE: 2001-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: FC-6-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brandt, Kevin S.
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 549
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                                                                                                                                                                                                                321 CAA 319
                               633 GAA 635
                                                               381
                                                                                              573
                                                                                                                            513 ATCAAAATTAGACGGTGCTAAAAACGCTCAAATTCATGGCGTTGGGCACATTGGTTTATT 572
                                                                                                                                                                                             501 TCAAAGTTATTTATTCTCAGTAAAACTCATTTTTAACAATATTAATCTTATGATATGTAA 442
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                                                                                                                                                                                                                                                             Local Similarity 49.7 nes 91; Conservative
                                                               GATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGGGGGGCCAAAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCGTGATTGATACCAAAATGA 5888
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                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaines, Patrick J.
Stinchcomb, Dan T.
Wisnewski, Nancy
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49.7%;
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Pred. No. 1;
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Pred. No. 0
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                                                                                                                                                                                                                                                                                              DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SEQ ID NO 3605
LENGTH: 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          561 CATTGGTTTATTGATGA 577
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APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATGATAAATGACCAAAATAGGTAAGTGATCAAAACAAGCAAAGTCTTTTCGTTTCGTC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAGATCAAACTCGTATGAGTAGTACCAAATCTGTTTGTCTATAGAACTTAAAACATAAG 106
                                                                                                                                                                                                    APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
                                                                                                                                                                                 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang,
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Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                       3.50 inch, 1.4Mb storage
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US-10-184-644-412
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                                                                                                                                                                                                                                                                                           SEQ ID NO 412
LENGTH: 546
TYPE: PRT
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Publication No.
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: U$/10/184,644
CURRENT FILLING DATE: 2002-66-28
Prior Application removed - See File Wrap
NUMBER OF SEO ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29643 CGCCGACAAATGGAGAAATCAAGAAGTGCAACAAGCAGAATAAGTTTTTTACAAAAATG 29584
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                                     365
                                                                                                     425 RY.MYGR...A..M..MNYN.R.Y..NA.NC....RT.DNRW.M.GA.YD.D..S.... 366
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                                                                                                                                              255 ATTATCACGATTTGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAAAAAAGTGGATATTGT 314
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REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
CGCTCACAGTATGGGTGGCGCGAACACACCTTACTACATAAAAAATCTGGACGGCGGAAA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTACAGCAGTGCCGATATGATTGTCATGAATTACTTATCAAAA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                   .AM.NNHM.H....ND.S..SD..Y..HGY....A.NTKMM.SN.B..MAC.NN.S.M. 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83;
                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 32768 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watanabe, Colin K. Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Godowski, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang,Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith, Victoria
                                                                                                                                                                                  Conservative
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                                                                                                                                                                                  96; Mismatches
                                                                                                                                                                                                 Score 33.8;
Pred. No. 2.3;
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Pred. No. 1
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US-10-184-634-412/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 412
LENGTH: 546
TYPE: PRT
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Matches
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrap
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhang, zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93430R1C217
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                                                                  ...M.HA.M.D.TY.N.Y..T.T.T..MTTADR.W..M.CA..T.S...ABH.....M.B
                                                                                                                                                                                                      .AM. NNHM.H....ND.S..SD..Y..HGY.....A.NTKMM.SN.B..MAC.NN.S.M. 306
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                                                                                                   TCCGGGAACAGATCCAAAACATTTTATACACATCCATTTACAGCAGTGCCGATAT 494
                                                                                                                                                                         CGCTCACAGTATGGGTGGCGCAACACCCTTACTACATAAAAAATCTGGACGGCGAAA 374
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                                                                                                                                     .DBCBHABB...MS.NSM.Y.BM.YM..Y.CH.B.RYNN.TS.NCA.D....AM.SR.W. 246
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...B.H.BAH..CS.K..D...MH.TNMA.Y.Y.MH.AW.NN.N..Y.MN.SB.S..BT.
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96; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Score 33.8;
Pred. No. 2.
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RESULT 12
US-10-147-467-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Molecular Toxicology Modeling FILE REFERENCE: 44921-5038-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Genbank Accession No. US20020119462A1 AI169239
                                                                               336
                                                                                                              303 AGTGGATATTGTCGCTCACAGTATGGGTGGCGCGAACACCACCTTACTACA 352
                                                                                                                                                        396
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                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US (FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/298,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/297,457
                                                                                                                                                        CAATAAATTTGCATTCTAACTTTCTTGGGAAAACATTTTTTGAAGAACCAGTAAGAAAAAC
                                                                           TGTAGATCTTACAGTTTACAGTTTGGTCACCTGCACAACATGTTACTAAA
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Elashoff, Michael
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ilarity 56.4%;
Conservative
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Pred. No. 3
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Sequence 1, Application US/10147467 Publication No. US20030027295A1 GENERAL INFORMATION:

APPLICANT: TAKESHI, IShii APPLICANT: SATOSHI, Mits

Mitsuda ESTERASE

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REFERENCE: 20-4336P

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                                                                                             RESULT 14
US-09-731-872-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-939-964-1
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US-09-939-964-1
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; TYPE: DNA
; ORGANIZSM: Burkholderia cepacia
US-10-147-467-1
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                                   GENERAL INFORMATION
                                                     Sequence 18, Application US/09731872 Patent No. US20020102604A1
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local
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CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 4
APPLICANT:
                 APPLICANT: Dumas Milne Edwards, Jean Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06-22
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APPLICANT: Freiberg, Christoph
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                                                                                                                                                                                                                                                                                   115 ATGGTTCACGGTATCGGAGGAGCTTCATACAATTTTGCGGGGAATTAAGAGCTATCTCGTA 174
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                                                                                                                                                                                                                                                ATCTTAGAGATGCTCGAAGAAGATATAAAGGATCTAGAGGGAGCGAGGCGAGAGCGCGTA 223336
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                                                                                                                                                                                                                                                                                                                                                                                                    88;
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Bougueleret,
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Broughton, William John
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Pred. No. 5.2;
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Sequence 1896, Application
Patent No. US20020146721A1
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OTHER INFORMATION: score 4.55778392992629
OTHER INFORMATION: seq LVLVKRLLAVSVS/CI
US-09-731-872-18
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Matches 62
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                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: 09/680,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Methods For Monitoring Multiple TITLE OF INVENTION: Expression FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS FILE REFERENCE: 78.US3.REG
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-03-27 NUMBER OF SEQ ID NOS: 8481
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/279,526
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Berka, Randy M. APPLICANT: Clausen, Ib Gi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                                                                                                                                                                                                                                          LENGTH: 432
TYPE: DNA
ORGANISM: Bacillus licheniformis
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NAME/KEY: CDS
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: sig_peptide
LOCATION: 94..210
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70
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                                                                       AAACTTCTAGGAATTATGATGACGATTATTTTGGCAATTGCTGTGTTGGGAACCGCTGCG
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Pred. No. 6.4;
0; Mismatches
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Pred. No. 11;
0; Mismatches
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37.8
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9609.021 Million cell updates/sec
AL068157 Drosophil
B1678753 SWS601 SW
AL760893 Arabidops
BG940033 ax03b04 f
A0989712 Rfc00339
BQ775177 UI-H-FH0-
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BG045372	BE554807	BE531285	CNS006TJ	BM468757	CNS012UB	AV788662	BM815886	BG319118	CNS0181N	CNS016QS	BQ719062	BH671466	AZ939720	BQ458269	BQ089146	BM965977	вм965989	AV536563	CNS013QR	AZ522069	CNS0183L	CNS02659	CNS005NL	вн607139	B1969075	AW544638	AZ356093	A2356293	AI457833	BQ458251	AQ991444	BM954950	вм954819	BQ079412	BQ741211	BG043888	BE555700	BQ253545	
G045372 Sv42b04.	E554807 sp81k	BE531285 601278207	L065906 Dr	68757	102029 Dr	88662	15886	19118 NXPV_023	08773	07086	9062	1466	9720	8269	9146	5977	5989	536563	197	9	ω	934	433	139	075	AW544638 C0184B02-	56093	AZ356293	7833	58251	4	54950	54819	79412	41211	43888	55700	53545	

## ALIGNMENTS

REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS RESULT 1 CNSOOL78 LOCUS COMMENT SOURCE ORGANISM DEFINITION JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila. CNS00L78 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR24B18 of RPCI-98 library from Drosophila melanogaster (fruit GSS. Genoscope. Direct Submission AL068157.1 The library is named RPCI-98 and was constructed genomic survey sequence. GI:4958085 DNA by partial

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RESULT 2
BI678753
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SWS601 SWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robinia pseudoacacia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                              126 Natural Resources, East Lansing,
Tel: 517 353 4751
                                                                                                                                                                                                                                                    Michigan State University
                                                                                                                                                                                                                                                                      Department of Forestry
                                                                                                                                                                                                                                                                                          Contact: Kyung-Hwan Han
                                                                                                                                                                                                                                                                                                            black locust (Robinia pseudoacacia) Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                             Han, K.-H., Yang, J., Park, S., Paule, C
Kamdem, D.P. and Keathley, D.E.
Analysis of gene expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta;
Rosidae; eurosids I; Fabales;
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                                  /organism="Robinia pseudoacacia"
/db_xref="taxon:35938"
/clone_lib="SWS (Sapwood of black locust -/cissue_type="sapwood"
/dev_stage="mature tree"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-98"
/note="end : TET3"
212 c 182 g
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/db_xref="taxon:7227"
/clone="BACR24B18"
                      /note="Vector:
                                                                                                                                                  Location/Qualifiers
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  The cDNA library was
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lambda TriplEx; Site_1: Sfi IA;
ibrary was made from the sapwood
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Fabaceae; Papilionoideae; Robi
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t - Summer) Robinia
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                                                                            Summer)"
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of a mature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 ACTAACAGCTCATTGATTCAGAATACAAATGCAAATAACAAAATGTAATCAAAATCCATA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAAAAAAATGAAAATTCAAATGACATTAATTAAAAAATCAAAAAT 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At2g19740. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    Plant Genomics program designated 'GABI'. Information availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (bases 1 to 628)
Li,Y., Strizhov,N.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A pipeline for automated high-throughput generation of FSTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler, and Weisshaar,B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosso, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL760893.1 GI:21501099
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new Arabidopsis thaliana T-DNA mutagenised population (GABI-Ka
                       214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 a
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                     a
                     removed"
                                                                                                                                               /Clone="GK-203F11-014507"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      black locust tree collected in Michigan in late July." 124 c 101 g 228 t 5 others
                                                                                  were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were
                                                               processed
                                                                                                                                                                                                                                                                                             /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                    /strain="Columbia
                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/strain="Columbia 0"
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                                                             for submission. T-DNA derived
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                                                             sequences were
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
National Institute of Diabetes and Digestive and Kidney Diseases
Deciding 10, Room 9B17, National Institutes of Health, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 354)
Gubin, A.N., Njoroge, J.M., Bouffard, G.G. and Miller, J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Intramural Sequencing Center (NISC).
Plate: 03 row: b column: 04
Seq primer: -40M13 forward primer (Amersham).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301 402 2373
Fax: 301 435 5148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene expression in proliferating human erythroid cells Genomics 59 (2), 168-177 (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jm7f@nih.gov
DNA Sequencing and analyses by National Institutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                         (Clontech) according to the manufacturer's protocol and cloned into EcoRI digested Lambda 2ap II vector
                                                                                          cytometric separation after a 5-day culture period in the presence of erythropoietin. Total RNA was purified from the sorted cell population using TRIzol reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's Capfinder CDNA Library Construction Kit
                                                                                                                                                                                         /note="Organ: blood; Vector: Lambda ZAP II; Site_1: EcoRI;
Site_2: EcoRI; 65,000 proliferating erythroid cells from
the buffy coat of a blood donation were obtained by flow
                                                                                                                                                                                                                                                                                     /cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ax03b04"
/clone_lib="Proliferating
                     (Stratagene). The phage library was to in vivo excision in SOLR cells. 1
                                                                                                                                                                                                                                                                                                                           /tissue_type="blood"
/cell_type="Erythroid Cells"
                                                                                                                                                                                                                                                /dev_stage="Progenitor;
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                  /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                        ibrary)
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A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                                                                                                                                                                                                                                                                                                                                              Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ989712 646 bp DNA linear GSS: Rfc00339 Photorhabdus luminescens strain W14 M13 library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biology and University of Bath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: ffrench-Constant
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(44) 1225 826621
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a 66 c 78 g 123 t
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                                                                                                                                                                     /strain="W14"
/db_xref="taxon:29488"
/clone="PLG00339"
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                                                                                        /note="Genomic DNA from strain W14 was size
                                                                                                                                      library'
                                                                                                                                                                                                                            /organism="Photorhabdus luminescens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-36, >AT_itch#Low_complexity (matched compliment)
280-325, >(TA)n#Simple_repeat (matched compliment) 636-702,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index Unpublished (1997)
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58; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: James Martin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D
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                 218
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                                                                                                                                                                                                              library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned
                                  TAG_SEQ=AGAATCCGGC"
                                                                                                                                        directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
                                                                                                                                                                                                                                                                                                       /lab_host="DH10B (Life Technologies)"
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FHO is a cDNA library containing the following tissue(s): Human Grade 1 Chondrosarcoma Cell Line The
                                                                    TAG_TISSUE=Human Chondrosarcoma
                                                                                       TAG_LIB=UI-H-FHO
                                                                                                        library is AGAATCCGGC. The ce
James Martin from University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="UI-H-FHO-bci-l-19-0-UI"
/clone_lib="NCI_CGAP_FHO"
                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Human Chondrosarcoma Cell Line'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: estéwatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further is
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,,R., Waterston,R., and Wilson,R.
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Washington University School of Medicine
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EST.
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                      XhoI; The Harosóy NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from whole seedlings
                                                                                                                                              /tissue_type="whole seedlings
/dev_stage="1 week old"
/lab_host="DH10B"
                                                                                                                                                                                                                      /clone="SOYBEAN CLONE ID:
/clone_lib="Gm-c1052"
                                                                                                                                                                                                                                                                      /organism="Glycine max"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                       /note="Vector: pBluescript II SK+; Site_1: EcoRI;
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grown plants.

Complementary DNA

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                                                                                                                                                                                                                                                                           Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                    est@watson.wustl.edu
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/tissue_type="Hypocoty1, 9-10 day old etiolated seedlings"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pBluescriptII SK+; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from etiolated hypocoty1 tissue of 9-10 day old seedlings
of the cultivar Williams 82. Complementary DNA was
                                                                                                                                       /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1045-1141"
/clone_lib="Gm-c1045"
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                                                                                                                                                                                                                                                                                                                                                               Email: estéwatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
Though: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-453 or contact via email: ccu@resgen.com
High quality sequence stop: 417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG043888 444 bp mRNA ]
saa34d09.yl Gm-c1059 Glycine max cDNA clone
ID: Gm-c1059-930 5', mRNA sequence.
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Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Public Soybean EST Project
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/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhOI; The cDNA library was constructed from mRNA isolated from 2 week old etiolated whole seedlings of pI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhOI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA
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/clone_lib="Gm-c1059"
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/db_xref="taxon:3847"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., J., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen
South Memorial Parkway Huntsville, AL 35801 For furt
call: (800)-533-4363 or contact: ccu@resgen.com web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
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BQ741211
BQ741211.1 GI:21887998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project
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synthesized from mRNA using a primer consisting of a poly(dT) primer with a XhoI restriction site: EcoRI adapters were ligated to the blunt-ended cDNA fragmu
                                                                      /note="Vector: pBluescriptII SK+; Site_1: EcoRI; Site_2: XhO; This cDNA library was constructed from mRNA isolate from etiolated hypocotyl tissue of 9-10 day old seedling of the cultivar Williams 82. Complementary DNA was
                                                                                                                                                                       /tissue_type="Hypocotyl, 9-10 day old etiolated seedlings"
/lab_host="DH10B"
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/clone_lib="Gm-c1045"
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/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ079412 503 bp mRNA 1 san1301.y1 Gm-c1084 Glycine max cDNA clone Gm-c1084-3626 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available through: ResGen, Inv
South Memorial Parkway Huntsville, AL 35801
call: (800)-533-4363 or contact: ccu@resgen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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Glycine max
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Phytophthora soyae race 1 and tissues were harvested 2 and 4 hours following infection. The library is the pool of these two time points. Complementary DNA was synthesized
                                                                /note-"vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was contructed by M. Bhattacharyya from mRNA isolated from etiolated hypocotyls from the cultivar Williams 82. Tissue was inoculated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restriction site of the \, pBluescript vector. The ligated cDNA fragments were transformed into DH10B \, host cells
                                                                                                                                                     /clone_lib="Gm-c1084"
/tissue_type="Etiolated hypocotyls
/lab_host="DH10B"
                                                                                                                                                                                                                          /clone="SOYBEAN CLONE ID: Gm-c1084-3626"
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                                                                                                                                                                                                                                                                  /organism="Glycine max"
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69.4%;
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301 For further i
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                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further ir
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 9-10 day old etiolated
                                                                     /clone="SOYBEAN CLONE ID: Gm-c1069-5289"
/clone_lib="Gm-c1069"
/tissue_type="Degenerating cotyledons, 9
etiolated seedling"
/lab_host="DH10B"
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SOURCE VERSION

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COMMENT

/note="Vector: pBluescript II SK+; Site\_1: EcoRI; Site\_2: XhoI; The cDNA library was constructed from mRNA isolated

TITLE

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                          Email: estéwatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                soybean.
Glycine max
                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                 Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                    www.resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shoemaker R/Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were
etiolated seedling"
/lab_host="DH10B"
                                                                /organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1069-5113"
/clone_Lib="Gm-c1069"
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                                                /tissue_type="Degenerating cotyledons, 9-10 day old
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                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel:
                                                                                                                                                                                                                                                                                                                                This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Biology and Biochemistry University of Bath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             South Building,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: ffrench-Constant RH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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A genomic sample sequence of the entomopathogenic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ffrench-Constant, R.H., Waterfield, N.,
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AQ991444.1 GI:9650038
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           170
                                                                                                                                                                                                                                                                                          primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                       (44) 1225 826621
(44) 1225 826779
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                                                                                                                                                                                                                                                                                                                                                                                                 bssrfc@bath.ac.uk
        Ω
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/note="Genomic DNA from strain W14 was size selected kb) and then cloned into M13 Janus."
194 c 124 g 167 t 6 others
                                                                                               library
                                                                                                                                                                                                        /organism="Photorhabdus luminescens"
                                                                       /dev_stage="primary phase variant"
                                                                                                                   /clone_lib="Photorhabdus luminescens strain W14
                                                                                                                                                           /db_xref="taxon:29488"
                                                                                                                                     /clone="PLG02380"
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at Washington University, St. Louis. Adult nematodes were colle
from infected dogs and provided by Dr. Prema Arasu of North
Carolina State University, Raleigh, NC (Prema_Arasu@ncsu.edu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Washington Univ. Nematode EST Project, 1999 Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toxocaridae; Toxocara.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: SL1 primer
                             187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allen, M., Person, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 525
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               est@watson.wustl.edu
                     were non-directionally cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning protocol. Adult nematodes were collected from infected dogs and provided by Dr. Prema Arasu of North Carolina State University, Raleigh, NC (Prema_Arasu@ncsu.edu)."
143 c 179 g 167 t
                                                                                                                                                                                 canis cDNA PCR products of size >400 nucleotides containing SL1 on the 5^{\prime} end and oligo(dT) on the 3^{\prime} end
                                                                                                                                                                                                                                   Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. Adult Toxocara
                                                                                                                                                                                                                                                                                /note="Vector: pCRII-TOPO (Invitrogen); Site_1: EcoRI;
Site_2: EcoRI; The library was constructed by Claire
                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Toxocara canis adult SL1 TOPO v1"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Toxocara canis"
/db_xref="taxon:6265"
                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 to 676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36.2; DE
Pred. No. 6.9;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Swaller, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Louis. Adult nematodes were collected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harvey, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schurk, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 30-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          James McCarter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kohn, S.
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Sear Job	Db	Qy	Db	Qy	Ъ	Qy .	рь	Qy
Search completed: May 18, 2003, 07:47:57 Job time: 1086 secs	352 TCGTCAGCTAATAATCGCTGTACGAGAGTATACGGGAA	279 TTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCG	292 TGACGGGGGCTCACAGAGGC	219 GGACAAGACAGGGACGAATT	Db 232 TCGTGAATATTTCATCAACATGGCTATTCGCCAGCCGAGCTTTACGCGACGACATATGG	159 TAAGAG	Db 172 AAAGACGCCAGTAGTGTTTGTGCATGGTGTTGCAACGACAGCGAATGTTTTCGTTAAGCA	99 /
	NAGCAAAAATGTGGATG 404	GCTCACAGTATGGGTG 331	ATTCGATGTACCGATCTTATGCAGATATATTCAACAGAT	TTATCACGATTTGTGCAAAAGGT 2	CAGCTTTACGCGACGACATATGG 2	PAAGCTGTATGCGGTTGATTTTTG 2	BACAGCGAATGTTTTCGTTAAGCA	AGCTTCATACAATTTTTGCGGGAAT 1
			351	278	291	18	231	158

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